Brooklyn Law Review

Volume 74 | Issue 2 Article 2

2008

Race, Genes and Justice: A Call to Reform the Presentation of Forensic DNA Evidence in Criminal Trials

Jonathan Kahn

Race, Genes, and Justice

A CALL TO REFORM THE PRESENTATION OF FORENSIC DNA EVIDENCE IN CRIMINAL TRIALS

Jonathan Kahn[†]

I. INTRODUCTION

How and when, if at all, is it appropriate to use race[1] in presenting forensic DNA evidence in a court of law? In October 2002, a California jury convicted William Curtis Wilson of "first degree murder with use of a dangerous weapon during commission of an attempted rape and a lewd act upon a child. The court sentenced him to a term of life in prison without possibility of parole."[2] DNA evidence played a central role in obtaining the conviction. This, in itself, is neither extraordinary nor unusual given the broad acceptance of the use of DNA evidence in courts across the country and, indeed, around the world.[3] The case is

---

[†] Associate Professor of Law, Hamline University School of Law. Ph.D., Cornell University; J.D., Boalt Hall School of Law. I would like to thank the participants of the Rutgers Center for Race and Ethnicity's Workshop on DNA, Race, and History and the M.I.T. Center for Race Diversity's conference on "What's the Use of Race" for their helpful comments on earlier drafts of this Article. I would also like to thank Simon Cole, Troy Duster, and Tom Romero for their comments, ideas, and suggestions that helped me along the way. Work on this Article was supported in part by the Ethical, Legal, and Social Implications Research Program, National Human Genome Research Institute (Grant number R03-HG004034-02).

[1] I do not attempt to provide a set definition of "race" in this Article. Rather, I focus primarily on how actors in specific legal and scientific contexts have used the term. In the interests of economy and manageable syntax, in the remainder of this Article I will often refer only to "race" when speaking generally of racial and ethnic categories. I am assuming both to be socially constructed categories that nonetheless have come to have biological implications as they play out in real world biomedical and forensic contexts. I will use the terms "race" and/or "ethnic" when referring to specifically marked groups. Thus, for example, the U.S. Census codes "White" or "Asian" as racial categories and "Hispanic" or "Latino" as ethnic categories. U.S. Census Bureau, Racial and Ethnic Classifications Used in Census 2000 and Beyond, http://www.census.gov/population/www/socdemo/race/racefactcb.html (last visited Sept. 22, 2008) [hereinafter Racial and Ethnic Classifications]. In the context of forensic practice, Hispanic is also sometimes referred to as a racial group. *See* Madeleine J. Hinkes, *Race, Ethnicity and Forensic Anthropology: Realities of Racial Determination in a Forensic Setting*, 13 NAT'L ASS'N FOR PRAC. ANTHROPOLOGY BULL. 48, 49 (1993) ("[O]ne's social race or 'ethnicity' may not be the same as [one's] biological race. For example, self-proclaimed 'Hispanic' individuals may be Spanish (Caucasoid), Mexican (American Indian), Puerto Rican (Negroid admixture), or Filipino (Asian Mongoloid)."). Ethnic groups are often also discussed as subgroups within races. For example, Italian or Irish might be understood as ethnic subgroups within the racial category of Caucasian.

[2] People v. Wilson (*Wilson I*), 21 Cal. Rptr. 3d 102, 106 & n.5 (Ct. App. 2004), *aff'd*, 136 P.3d 864 (Cal. 2006).

[3] The literature on the development and current state of the use and acceptance of DNA for forensic purposes is extensive. Helpful resources for exploring some of these issues can be found

noteworthy, however, for its discussion of the appropriate use of racially identified forensic DNA databases in calculating the odds that DNA left at the scene of the crime by the perpetrator might be that of the defendant. The crime scene DNA was found to match the defendant Wilson's DNA at nine distinct loci, or specific points on the genome.[4] The question then became what were the odds that someone else might share the defendant's same genetic profile? Such odds are known as a Random Match Probability (RMP)—the probability of finding the same DNA profile identified in the crime scene sample in a randomly selected, unrelated individual.[5]

The California Supreme Court noted that RMP calculations by Nicola Shea, a California Department of Justice criminologist,[6] provided support for the conclusion that Wilson's "genetic profile would be expected to occur in one of 96 billion Caucasians, one of 180 billion Hispanics, and one of 340 billion African-Americans" and that "these profiles were extremely rare; [after all,] the world contains only about six and a half to seven billion human beings."[7] On appeal to the California Court of Appeal, Wilson's attorneys strenuously contested this use of race-specific DNA databases to calculate odds to assist the trier of fact in reaching a verdict.[8] Invoking the 2003 Court of Appeal for the Fifth District decision in *People v. Pizarro*,[9] they argued that the presentation of such race-specific odds was permissible *only* when the race of the *perpetrator* was known.[10] Otherwise, they contended, the use of such evidence lacked sufficient evidentiary foundation because it was based on the improper assumption that the defendant was in fact the perpetrator.[11] In July 2006, the California Supreme Court rejected this argument, finding that the introduction of evidence of the odds of a DNA match calculated using race-specific databases from major racial or

---

at web sites maintained by the National Conference of State Legislatures and by the President's DNA Initiative. *See generally* National Conference of State Legislatures, DNA in Criminal Justice (Aug. 28, 2008), http://www.ncsl.org/programs/cj/dna.htm; The President's DNA Initiative, Advancing Justice Through DNA Technology, http://www.dna.gov (last visited Sept. 22, 2008). For a brief history of the development and use of forensic DNA technologies, see JOHN M. BUTLER, FORENSIC DNA TYPING: BIOLOGY, TECHNOLOGY, AND GENETICS OF STR MARKERS 1-13 (2d ed. 2005).

[4] *Wilson I*, 21 Cal. Rptr. 3d at 105, 114.

[5] *See* BUTLER, *supra* note 3, at 481, 486-88. That the individual is "unrelated" is significant because related individuals will have a higher likelihood of sharing a greater percentage of DNA, hence altering the probabilities of a random match. *See id.*

[6] People v. Wilson (*Wilson II*), 136 P.3d 864, 866 (Cal. 2006).

[7] *Id.* at 867.

[8] *Wilson I*, 21 Cal. Rptr. 3d at 106.

[9] 3 Cal. Rptr. 3d 21 (Ct. App. 2003), *disapproved by* People v. Wilson, 136 P.3d 864 (Cal. 2006).

[10] *See* Appellant's Opening Brief on the Merits at 25-26, People v. Wilson, 136 P.3d 864 (Cal. 2006) (No. S130157).

[11] *Id.* at 24; *see also Wilson II*, 136 P.3d at 867, 872.

ethnic groups represented in the local population was acceptable—thereby effectively overturning the recent ruling in *Pizarro*.[12]

Paired together, the holdings in *Pizarro* and *Wilson* provide a relatively bounded and focused site for the examination of debates relating to the use of racialized databases in forensic DNA analysis.[13] *Pizarro* involved an appeal from a case originally tried in 1990, when forensic DNA testing was still in its infancy. At the original trial, the forensic expert for the state testified that the odds of the defendant's genetic profile occurring in other population groups ranged from one in 250,000 in "Hispanics" up to one in 10,000,000 in "Caucasians"[14] (frequencies in other racial populations were not presented to the jury).[15] Here, the difference produced by using racially marked databases may be significant—not only statistically, but also as a legal matter. The lower denominators in this situation may be understood in large part as a function of the more rudimentary techniques for DNA analysis at the end of the 1980s.[16] Race seemed relevant because it appeared to refine the

---

[12] *Wilson II*, 136 P.3d at 873.

[13] At the outset, it is important to note that these questions are distinct from (yet ultimately related to) current heated debates concerning the use of DNA technologies to construct racial profiles of potential suspects from DNA samples left by an unknown perpetrator at the scene of a crime. *See generally* Frederick R. Bieber, *Science and Technology of Forensic DNA Profiling: Current Use and Future Directions*, *in* DNA AND THE CRIMINAL JUSTICE SYSTEM: THE TECHNOLOGY OF JUSTICE 23 (David Lazer ed., 2004); Pilar N. Ossorio, *About Face: Forensic Genetic Testing for Race and Visible Traits*, 34 J.L. MED. & ETHICS 277, 281-83 (2006). Such technology is largely *prospective*, being used in law enforcement contexts by investigating police authorities. It uses race to aid in the apprehension of a possible suspect. *See* Bieber, *in* DNA AND THE CRIMINAL JUSTICE SYSTEM: THE TECHNOLOGY OF JUSTICE, *supra*, at 36-38. In contrast, the use of race-specific databases at trial is largely *retrospective*. It is used by prosecutors to link an already apprehended suspect back to the crime by matching his or her DNA to a sample found at the crime scene. *See* Edward J. Imwinkelried, *The Relative Priority that Should Be Assigned to Trial Stage DNA Issues*, *in* DNA AND THE CRIMINAL JUSTICE SYSTEM: THE TECHNOLOGY OF JUSTICE, *supra*, at 91, 97-100. The basic technology used is also often different. As discussed further below, courtroom uses of DNA involve constructing statistical probabilities for matches between two existing samples of DNA—the defendant's and the crime scene sample. *See infra* Parts II.A-B. Racial profiling for unsolved crimes generally involves examining a crime scene DNA sample for "Ancestry Informative Markers" (AIMS), which (though highly controversial) are believed by some scientists to provide indications of the likely ancestry, or mixture of ancestries, of the human source of the sample. *See, e.g.*, Mark Shriver et al., Commentary, *Getting the Science and the Ethics Right in Forensic Genetics*, 37 NATURE GENETICS 449, 449-50 (2005). For a critique of this technology in the forensic context, see generally Mildred K. Cho & Pamela Sankar, Commentary, *Forensic Genetics and Ethical, Legal and Social Implications Beyond the Clinic*, 36 NATURE GENETICS S8 (2004) [hereinafter *Forensic Genetics*]; Mildred K. Cho & Pamela Sankar, Response, *Getting the Science and the Ethics Right in Forensic Genetics*, 37 NATURE GENETICS 450, 450-51 (2005). These technologies and their forensic uses, though in many respects different, do share a common propensity to reify race as genetic. Such a propensity is socially dangerous and threatens to recreate or revitalize stigmatized conceptions of biologically superior and inferior races. *See, e.g.*, Troy Duster, *Race and Reification in Science*, 307 SCIENCE 1050, 1050-51 (2005); Sandra Soo-Jin Lee et al., *The Meaning of "Race" in the New Genomics: Implications for Health Disparities Research*, 1 YALE J. HEALTH POL'Y L. & ETHICS 33 *passim* (2001). Such a propensity is also scientifically suspect, is based on highly problematic assumptions about the correlations between race and biological ancestry, and disregards current, broadly held understandings of the incoherence of race as a genetic concept. *See infra* notes 122-127 and accompanying text; *see also infra* Part V.B.

[14] *Pizzaro*, 3 Cal. Rptr. 3d at 97-98.

[15] *Id*. at 104 n.81.

[16] *See* BUTLER, *supra* note 3, at 2-6.

results of a newly developing and still relatively crude technology. Hence, race became instantiated at the outset of forensic DNA analysis as a basic framework for presenting data. By the time of Wilson's case, however, the technology had developed to such an extent that it was regularly capable of producing odds ratios on the order of one in the hundreds of billions.[17] With such odds, the practical utility of distinguishing RMPs by race disappears. Nonetheless, race has remained ingrained in the framework of the production and interpretation of forensic DNA evidence.[18]

This Article considers how relations between science and law must continually be reevaluated in light of changing social and technological developments. It questions the underlying assumption of the utility of race itself in forensic DNA analysis. Beginning with a review of the development of forensic DNA technology, it examines what race adds as a practical matter to the ability of a finder of fact to make fair and accurate decisions. Any such value must then be weighed against the potential dangers of bias created by introducing issues of race as genetic into the context of what is usually a violent crime. The Article argues that in most cases such evidence should be excluded as irrelevant or that, if deemed relevant, it should be held inadmissible because the dangers of infecting the proceedings with racial prejudice outweigh any possible benefit that introducing the race-based statistics could provide. This is not necessarily because the mere mention of race will inevitably taint a jury's deliberations, but rather because the benefits of using race in such a context must be deemed so de minimis as to be incapable of outweighing even a remote danger of racial prejudice. Moreover, when examining the implications of connecting race and genetics in the context of violent crime, this Article will consider that oftentimes such a danger may be far from remote. The Article concludes that in most cases, given the current state of forensic DNA technology, there is no longer any justification (if there ever was any) for using race-specific databases in presenting DNA evidence to a jury. Ironically, given the power of current technology to generate powerful RMPs, adopting the recommendation to abandon the use of race in the presentation of forensic DNA evidence would not materially affect the ability of prosecutors to obtain convictions based on DNA evidence. It would, however, transform the way in which race, genes, and violent crime are associated in the criminal justice system.

The Article reaches this conclusion by first providing background, in Part II, to the history and technical aspects both of forensic DNA analysis and of debates regarding the relation between

---

[17] *See, e.g.*, *id.* at 8-10; Bruce Budowle et al., *Source Attribution of a Forensic DNA Profile*, 2 FORENSIC SCI. COMM., July 2000, *available at* http://www.fbi.gov/hq/lab/fsc/backissu/july2000/source.htm#Introduction.

[18] *See infra* Parts IV.C-D.

race and genetics. This section begins by introducing some of the details of early forensic DNA practices and procedures. It also examines early debates over the appropriate use of racial categories in generating statistical match probabilities. In the early years of forensic DNA analysis, the late 1980s and early 1990s, these debates did not involve questions of *whether* to use race, but rather *how much* race to use. The concern of some early forensic DNA analysts was that using too broad a population group would generate odds of a match that were unfairly low. Advocates of using broad racial categories argued that such categories provided a pragmatic and useful means to generate more accurate statistics rather than using an undifferentiated general population database, while still providing odds that were fair to a defendant. Critics of this approach argued that since there is more genetic variation within racial groups than between them, databases should be characterized by smaller subgroups within the larger racial designation in order to provide even better information about RMPs. This Part of the Article also considers how these arguments relate to broader issues concerning the nature of race in relation to genetics. This Part concludes with an examination of how the debates over using race to calculate RMPs were ultimately settled by the mid-1990s in favor of using broad racial categories, which then became the norm for forensic DNA practice in the United States.[19]

Part III examines the current standards and protocols for conducting forensic DNA analysis and considers how, where, and when forensic experts inject race into their practices. This section begins with an examination of DNA databases, focusing on the FBI's Combined DNA Index System (CODIS), which began as a pilot project in 1990 and has since evolved into a major database of over five million DNA profiles from convicted offenders nationwide.[20] It reviews technological developments that have greatly increased the power and efficiency of forensic DNA analysis and considers the selection of thirteen genetic loci that have become the standard for generating DNA matches and calculating RMPs.[21]

Part IV contrasts the elaboration and standardization of such technical protocols for DNA analysis with the protocols (or lack thereof) for producing and using racial and ethnic categories in forensic DNA analysis. Here, I argue that the use of racial categories is woefully under-conceptualized and wholly inadequate—especially when contrasted with the great care taken to elaborate the technical protocols for DNA analysis itself. I argue that similar care of the data should be given to methods for using racial categories in a genetic context. I put forward the use of general, non-racial reference population databases as the obvious

---

[19] *See infra* Part II.C.

[20] *See infra* notes 151-154 and accompanying text.

[21] *See infra* text accompanying notes 145-153.

solution to this problem. This Part concludes with a recommendation that what I call the "inertial power of race" has remained in a system of practice and analysis long after the initial reasons for using it have faded. It considers, as well, some of the dangers, beyond the court room, of allowing race to persist in a context that inappropriately reifies it as genetic.

Part V returns to *People v. Wilson* and related cases to examine the current state of how race is used in presenting forensic DNA data in courts of law. The focus here is primarily on developments in California case law as a case study that provides a particularly good site of analysis and raises issues that are relevant to understanding how racialized data is used in presenting DNA evidence in courts across the country. A close analysis of these cases provides a clear and factually specific context for understanding broader issues of how and why racialized genetic data is used in today's criminal justice system.

Part VI develops a specific critique of current uses of racialized DNA evidence and elaborates on (or expands) the argument that, in most cases, race-specific genetic data that is used to generate RMPs should not be admitted in court. This section begins with a brief consideration of the court's gate-keeping function in evaluating scientific evidence under *Daubert v. Merrell Dow Pharmaceuticals, Inc*.[22] Using the Federal Rules of Evidence ("FRE") as a framework, it then considers the basic question of what race adds to RMPs generated through forensic DNA analysis. More specifically, given that it is possible, with current technology, to generate astronomically low RMPs without using race, it questions whether any legally relevant information of practical use to the finder of fact is added by introducing race into the calculation. The problem here is to consider whether such data passes the threshold for legal relevance in determining its admissibility. Here, I assert that courts must be careful to distinguish between statistical relevance and legal relevance in evaluating such evidence. I argue that in many situations the different RMPs produced by referencing distinct race-specific databases provide no useful additional information to the trier of fact and so should be excluded. I conclude that the only thing race adds to the proceedings is race itself. It associates race, genes, and violent crime in a manner wholly irrelevant to the determination of a particular defendant's guilt or innocence.

I then move on to argue that even if such evidence is deemed relevant, it should nonetheless be excluded as prejudicial. Here, I weigh any possible benefits to using race-specific RMPs in presenting evidence against the dangers of injecting the proceedings with unfounded associations of race, genes, and crime, which threaten to evoke attitudes among the jury that, even if unconscious, are improperly tainted with racism. In developing this section, I consider studies that examine the

---

[22] 509 U.S. 579 (1993).

particular psychology involved in presenting DNA evidence to a jury. Further, I bring that work into dialogue with studies on the psychology of implicit prejudice—tacit attitudes towards race that are often held without an individual's own conscious awareness of how they influence his or her perceptions of and responses to racialized subjects. Together, the persuasive authority of DNA evidence and the reality of implicit prejudice call into question the legitimacy of using racialized DNA evidence.

Concern over the prejudicial impact of such evidence gains added force when we situate those rather abstract psychological dynamics of implicit prejudice within the context of the highly racialized nature of the current or today's United States' criminal justice system. Here, I argue that the pervasive racialization of violent crime in the United States takes such concerns out of the realm of mere speculation and gives concrete cause for concern. Given the de minimis nature of any possible practical utility to be gained from introducing race-specific RMPs in most cases, I conclude that the prejudicial potential of such evidence clearly outweighs any possible benefits it might provide.

The Article concludes with a brief synthesis of the arguments for ending the practice of using race to frame the presentation of forensic DNA evidence. It notes that this would not materially hinder the ability of prosecutors to obtain convictions using DNA evidence. Yet, by removing the gratuitous introduction of race into a context of genetics and violent crime, such reform would promote a positive and significant reorientation of the relation among race, genes, and justice.

II. RACE AND THE EARLY DEVELOPMENT OF FORENSIC DNA

A. Origins of Forensic DNA Testing

DNA is made up of sequences of four nucleotides: adenine, cytosine, guanine, and thymine—commonly represented as A, C, G, and T.[23] Each nucleotide base is paired through a process known as hybridization: A is always paired with T; C is always paired with G.[24] The human genome has roughly three billion of these "base pairs."[25] There are two major steps in using DNA for purposes of forensic identification. First, a sample left at the crime scene by the perpetrator is compared to a sample from a suspect.[26] Second, if there is a "match,"

---

[23] National Human Genome Research Institute, A Brief Guide to Genomics, http://www.genome.gov/18016863 (last visited Sept. 18, 2008).

[24] *Id.*; National Human Genome Research Institute, Talking Glossary, http://www.genome.gov/glossary.cfm?key=hybridization (last visited Sept. 18, 2008) (defining hybridization).

[25] BUTLER, *supra* note 3, at 20. For a helpful review of these general scientific concepts in a forensic context, see *id.* at 18-20.

[26] David H. Kaye, *DNA Evidence: Probability, Population Genetics, and the Courts*, 7 HARV. J.L. & TECH. 101, 104 (1993).

then statistics must be used to calculate the frequency of that DNA "profile" in an appropriate reference population.[27] This latter step is required because, although every person's DNA is unique, it is impractical to compare the full three billion nucleotide base pairs of two samples for forensic purposes.[28] Therefore, two samples will be compared only at a limited set (usually between four and thirteen) of "loci," or specific parts of the genome.[29] For this practice to be effective, it is necessary to find loci that are highly variable between individuals and test only for them.[30] Humans, however, are essentially identical in about 99.5% of their DNA.[31] Finding the specific points of variation among individuals, therefore, can be difficult.[32]

In 1985, English geneticist Alec Jeffreys first described a method for developing a DNA "profile" of a person in a manner that might be used for purposes of forensic identification.[33] Jeffreys' innovation consisted of observing that, in particular regions of the human genome, short segments of DNA—the ACGT nucleotide sequence—are repeated between twenty and one hundred times.[34] These regions of the genome are called "variable number of tandem repeats," or VNTRs.[35] Different numbers of these repeats compose VNTR "alleles," which are also known as variations.[36] In order to examine and visualize the VNTRs, Jeffreys employed a technique known as restriction fragment length polymorphism (RFLP), which involves cutting the DNA near the VNTRs with an enzyme.[37] By looking at VNTRs from several distinct loci on the genome, it is possible to calculate the probability that a particular genetic profile comprised of distinct sets of VNTRs will appear in one or more individuals in a particular population.[38] For example, "[a] standard way to estimate frequency [of a particular profile] is to count occurrences in a random sample of the appropriate population and then use classical statistical formulas to place upper and lower confidence limits on the

---

[27] *Id.*

[28] *Forensic Genetics*, *supra* note 13, at S9.

[29] *See* BUTLER, *supra* note 3, at 2-6, 94.

[30] *Id.* at 2-6.

[31] Older analyses typically put the figure at 99.9%, but a more recent study indicates that 99.5% may be a more accurate finding. *See* Rick Weiss, *Mom's Genes or Dad's? Map Can Tell*, WASH. POST, Sept. 4, 2007, at A01, *available at* http://www.washingtonpost.com/wp-dyn/content/article/2007/09/03/AR2007090301106_2.html.

[32] *See* BUTLER, *supra* note 3, at 2-6.

[33] *See generally* Alec J. Jeffreys et al., *Hypervariable "Minisatellite" Regions in Human DNA*, 314 NATURE 67 (1985); s*ee also* NAT'L COMM'N ON THE FUTURE OF DNA EVIDENCE, NAT'L INST. OF JUSTICE, THE FUTURE OF FORENSIC DNA TESTING: PREDICTIONS OF THE RESEARCH AND DEVELOPMENT WORKING GROUP 14-15 (2000), *available at* http://www.ncjrs.gov/pdffiles1/nij/183697.pdf [hereinafter FUTURE].

[34] BUTLER, *supra* note 3, at 2-3; R.C. Lewontin & Daniel L. Hartl, *Population Genetics in Forensic DNA Typing*, 254 SCIENCE 1745, 1745 (1991).

[35] BUTLER, *supra* note 3, at 2-3.

[36] Lewontin & Hartl, *supra* note 34, at 1745.

[37] BUTLER, *supra* note 3, at 2-3.

[38] *Id.* at 2-3, 623-24.

estimate."[39] The resulting "conclusion[] of identity or nonidentity between two samples [is therefore necessarily] probabilistic."[40] In conducting the comparison, investigators came to adopt the "product rule"[41] for determining RMPs.[42] Any given VNTR may be calculated to occur at a certain frequency in a random population.[43] By the early 1990s, the standard was to test for VNTRs at four independent loci on the genome.[44] The product rule allows for multiplying each independent genotype frequency together to produce an overall probability of a match at all four loci.[45]

Jeffreys' innovation was first used in a forensic setting in England in 1986.[46] Forensic DNA testing was first used in the United States in 1987.[47] Shortly thereafter, commercial laboratories began practicing the "fingerprinting" procedure, and the U.S. Federal Bureau of Investigation began using forensic DNA techniques.[48] Critical to the acceptance of forensic DNA in courts was the development of standards of technical proficiency and accuracy in generating RMPs.[49] The product rule was one such standard, requiring that each chosen loci be understood as being inherited independently of the others.[50] Also important were basic crime scene management techniques for the identification and handling of DNA samples.[51]

---

[39] NATIONAL RESEARCH COUNCIL, DNA TECHNOLOGY IN FORENSIC SCIENCE 9 (1992) [hereinafter NRC I].

[40] *Forensic Genetics*, *supra* note 13, at S9; *see also* Lewontin & Hartl, *supra* note 34, at 1745-46.

[41] Richard Lempert defines the product rule as follows:

> According to the product rule, the probability of two independent events equals the probability of the first event times the probability of the second; with *n* independent events the separate probabilities of each of the *n* events are multiplied together to give the probability of their joint occurrence. Thus if the probability that a person had allele A = 1/10 and the probability that he had allele B = 1/10 and the probability that he had allele C = 1/10, and if the probability that the person had one of these alleles was not affected by whether or not he had either or both of the others, the probability that the person would have alleles A, B, and C would be 1/10 x 1/10 x 1/10, or 1/1000.

Richard Lempert, *The Suspect Population and DNA Identification*, 34 JURIMETRICS J. 1, 1 n.3 (1993).

[42] BUTLER, *supra* note 3, at 480-82, 485-86; Lewontin & Hartl, *supra* note 34, at 1746.

[43] *See* Lewontin & Hartl, *supra* note 34, at 1746.

[44] *See* BUTLER, *supra* note 3, at 2-3; Kaye, *supra* note 26, at 107.

[45] *See* Lewontin & Hartl, *supra* note 34, at 1746.

[46] BUTLER, *supra* note 3, at 3.

[47] Tracey Maclin, *Is Obtaining an Arrestee's DNA a Valid Special Needs Search Under the Fourth Amendment? What Should (and Will) the Supreme Court Do?*, 34 J.L. MED. & ETHICS 165, 165 (2006).

[48] FUTURE, *supra* note 33, at 15.

[49] *See, e.g.*, Lempert, *supra* note 41, at 1-3; *Forensic Genetics*, *supra* note 13, at S9.

[50] *See* Lempert, *supra* note 41, at 1; *see also* D. H. Kaye, *Logical Relevance: Problems with the Reference Population and DNA Mixtures in* People v. Pizarro, 3 L. PROBABILITY & RISK 211, 211-15 (2004) [hereinafter *Logical Relevance*].

[51] This latter area of concern was brought front and center in 1995 in the highly publicized murder trial of O. J. Simpson, where defense lawyers undermined apparently airtight evidence connecting Simpson to the crime by calling into question the methods (or lack thereof)

B. Early Questions and Challenges: DNA Evidence and Race Debated in the Courtroom, National Studies, and Scholarly Journals

Questions about the reliability of DNA evidence surfaced as early as 1989 in cases such as *People v. Castro*[52] in New York and *State v. Schwartz*[53] in Minnesota. Partially in response to these cases, several federal agencies urged the National Research Council (NRC) of the National Academies of Science (NAS) to study and recommend guidelines for the production and use of DNA evidence.[54] The NRC created a Committee on DNA Technology in Forensic Science, which issued a report in 1992.[55] It is in the context of the production of this report that race first enters the story front and center.

The Committee covered an array of issues relating to the forensic use of DNA technologies.[56] Among its most controversial findings were those relating to reference populations and the appropriate methodology for calculating RMPs.[57] In order to calculate the odds of any particular VNTR allele appearing at a given locus on the genome, one must have an appropriate reference population.[58] The product rule depends on the assumption of statistical independence of the alleles tested—that is, that they do not tend to occur in groups.[59]

Generally speaking, the more "related" a person is to a particular population group, the higher the odds are of finding shared alleles—or, alternatively stated, the less independence there is among alleles.[60] Siblings would likely share more DNA than cousins; cousins more than others in the same isolated village; members of the same isolated village more than others in the same region; and so forth. Higher odds favor a suspect or defendant because they indicate a greater likelihood that some other person may have left the DNA sample found at a particular crime scene.[61] The choice of reference population, therefore, can play a critical

---

employed by the Los Angeles Police Department in the collecting and handling of relevant DNA samples. *See, e.g.*, David Lazer, *Introduction: DNA and the Criminal Justice System*, *in* DNA AND THE CRIMINAL JUSTICE SYSTEM: THE TECHNOLOGY OF JUSTICE, *supra* note 13, at 3, 4; Sheila Jasanoff, *DNA's Identity Crisis*, *in* DNA AND THE CRIMINAL JUSTICE SYSTEM: THE TECHNOLOGY OF JUSTICE, *supra* note 13, at 337, 340-45.

[52] 545 N.Y.S.2d 985, 993 (Sup. Ct. 1989).

[53] 447 N.W.2d 422, 426 (Minn. 1989).

[54] Jasanoff, *supra* note 51, at 339-40.

[55] *See generally* NRC I, *supra* note 39.

[56] *See generally id.* The report was particularly concerned with exploring issues related to insuring the technical accuracy of RMPs and errors that might occur through sample collection, handling, and statistical methods.

[57] For an excellent discussion of the NRC I report and the subsequent controversies about its findings, see JAY D. ARONSON, GENETIC WITNESS 153-71 (2007).

[58] NRC I, *supra* note 39, at 10-13, 75-82; Kaye, *supra* note 26, at 137-38.

[59] *See* NRC I, *supra* note 39, at 11.

[60] *See id.* at 79.

[61] *See* Lempert, *supra* note 41, at 5-7; NRC I, *supra* note 39, at 79-80.

role in shaping the weight and authority of DNA evidence.[62] The choice, however, is not always straightforward. Indeed, some of the earliest and most contentious controversies involving the use of DNA technology in forensic science involved choosing the appropriate population against which a suspect's DNA should be compared and defining just how the suspect may be "related" to this population.[63] Concepts of race played a central role in these debates and continue to frame the way forensic scientists, law enforcement, and the bar produce and interpret DNA evidence to this day.[64]

The basic issue is whether or to what extent racial or ethnic categories should be used to characterize reference populations against which particular DNA samples could be compared to generate RMPs. The use of such categories may be particularly problematic in the arena of forensic DNA analysis because racial groups, especially those delineated in the U.S. Census, are fundamentally *social*, not *biological*, categories.[65] Indeed, at least since the 1970s scientists have understood that race will statistically explain only a small portion of genetic variations.[66] As a recent editorial in *Nature Genetics* put it, "scientists have long been saying that at the genetic level there is more variation between two individuals in the same population than between populations and that there is no biological basis for 'race.'"[67] Nonetheless, to the extent that certain population geneticists understand particular racial groups as sharing a common genetic ancestry—usually by using race as a crude surrogate for geographic or continental ancestry—members of those groups can be viewed as more "related" to each other (like an extended family) than to individuals from other groups.[68] This problematic understanding of relatedness can then affect the calculation of RMPs. Generally speaking, the more fine-grained the

---

[62] *See* NRC I, *supra* note 39, at 75-85; *Forensic Genetics*, *supra* note 13, at S9.

[63] *See generally* BUTLER, *supra* note 3, at 455-517.

[64] *See, e.g.*, ARONSON, *supra* note 57, at 120-45; *Forensic Genetics*, *supra* note 13, *passim*; Ossorio, *supra* note 13, *passim*.

[65] For example, federally mandated racial and ethnic categories are not biomedical in origin. Revisions to the Standards for the Classification of Federal Data on Race and Ethnicity, 62 Fed. Reg. 58,782, 58,782 (Oct. 30, 1997), *available at* http://www.whitehouse.gov/omb/fedreg/ombdir15.html. Rather, they derive from the 1997 Office of Management and Budget's (OMB) "Revisions to the Standards for the Classification of Federal Data on Race and Ethnicity." *Id.* The OMB standards set forth "five minimum categories for data on race: American Indian or Alaska Native, Asian, Black or African American, Native Hawaiian or Other Pacific Islander, and White." *Id.* There are "two categories for data on ethnicity: 'Hispanic or Latino,' and 'Not Hispanic or Latino.'" *Id.* These categories provide the basis for the classification of all federal data on race and ethnicity, most notably, the census. The OMB Standards, however, contain an important caveat: "The racial and ethnic categories set forth in the standards should not be interpreted as being primarily biological or genetic in reference." *Id.* These categories were developed to serve social, cultural, and political purposes. *Id.* at 58,782-83.

[66] Richard C. Lewontin, *The Apportionment of Human Diversity*, 6 EVOLUTIONARY BIOLOGY 381, 381-82, 296-97 (1972).

[67] Editorial, *Genes, Drugs and Race*, 29 NATURE GENETICS 239, 239 (2001).

[68] *See, e.g.*, Neil Risch et al., *Categorization of Humans in Biomedical Research: Genes, Race and Disease*, GENOME BIOLOGY, July 1, 2002, at 1, 3.

characterization of a particular reference population, the higher the odds of a random match,[69] higher odds again favoring the suspect or defendant. In the early years of forensic DNA analysis, when typically only four VNTR loci were tested, there were concerns that using a general, undifferentiated population database would produce inappropriately low RMPs.[70] The decision to use race in constructing and categorizing reference populations was introduced into forensic DNA analysis with the belief that it would improve the precision of the calculations that generate RMPs.[71]

In early 1991, two pairs of eminent population geneticists squared off against each other in the pages of *Science*, a highly influential scientific journal, to debate the problem of using racial categories in forensic DNA analysis.[72] On one side were Professors Richard Lewontin of Harvard University and Daniel Hartl of the University of Washington.[73] On the other side were Ranajit Chakraborty of the University of Texas and Kenneth Kidd of Yale University.[74] Their dispute did not revolve around the question of *whether* to use race but rather *how much* race to use in constructing reference population databases from which to calculate match probabilities.[75]

Lewontin and Hartl questioned the then-current practice of calculating allele frequencies in the racial categories used in the Census such as "Caucasian," "Black," and "Hispanic" to provide the basis for calculating RMPs.[76] They argued that such groupings were too broad and that substantial "genetic substructur[ing]" occurred *within* the broad racial groupings that should be taken into account in calculating match probabilities.[77] Using these broad racial groupings could produce RMPs with substantially lower odds than those that might be produced using more fine-grained ethnically identified subpopulations.[78] These concerns grew logically out of Lewontin's earlier path-breaking work showing how genetic variation *within* socially identified racial groupings was actually greater than variation observed *between* such groups.[79] This work laid the foundations for understanding that race was incoherent as a

---

[69] *See* Lewontin & Hartl, *supra* note 34, at 1748-49; *see also* NRC I, *supra* note 39, at 10-13.

[70] *See* ARONSON, *supra* note 57, at 120-45.

[71] *Forensic Genetics*, *supra* note 13, at S9.

[72] *See generally* Ranajit Chakraborty & Kenneth K. Kidd, *The Utility of DNA Typing in Forensic Work*, 254 SCIENCE 1735, 1735-37 (1991); Lewontin & Hartl, *supra* note 34, at 1746.

[73] Lewontin and Hartl were described by an editorial accompanying the article as "two of the leading lights of population genetics." Leslie Roberts, *Fight Erupts Over DNA Fingerprinting*, 254 SCIENCE 1721, 1721 (1991).

[74] Chakraborty & Kidd, *supra* note 72, at 1735.

[75] ARONSON, *supra* note 57, at 139-45.

[76] Lewontin & Hartl, *supra* note 34, at 1747.

[77] *Id.*

[78] *Id.*

[79] Lewontin, *supra* note 66, at 381.

genetic concept, or at best, an overly crude surrogate for genetic variation that improperly tended to reify race as genetic.[80] Thus Lewontin and Hartl observed that

> [a]mong genes that are polymorphic in European national or ethnic groups, the magnitude of the differences in allele frequency among subpopulations differs from one gene to the next. . . . For example, there are striking geographical clines of allele frequency across Europe for the ABO blood groups: the frequency of the B allele is 5 to 10% in Britain and Ireland, increases across Eastern Europe, and reaches 25 to 30% in the Soviet Union; the frequency of the O allele is 70 to 80% in Sardinians, Irish, and Scottish populations but lower in Eastern European populations. These clines reflect the migrations and political history of Europe over the last few thousand years.[81]

Problems were even greater for the "heterogeneous assemblage" known as the "Hispanic" population, which presented "perhaps the worst case for calculating reliable probabilities."[82] Consequently, Lewontin and Hartl concluded that using reference databases organized by the broad racial groupings "Caucasian," "Black," and "Hispanic" was unjustified.[83]

Chakraborty and Kidd argued that Lewontin and Hartl exaggerated both the extent of ethnic substructuring in America and its significance for calculating match probabilities.[84] While conceding that some substructuring existed, they argued that its effects upon frequency estimates generated by using the broader racial databases were "trivial."[85] Chakraborty and Kidd did not deny that using finer-grained ethnic reference populations might produce more precise allele frequency estimates.[86] Rather, their point was that such an approach was unnecessary—and unnecessarily burdensome. Current technology and understandings of population genetics, they asserted, justified the use of broad racial and ethnic categories, which were, additionally, far more practical and currently available.[87] Race was at the center of this early debate. But again, for these eminent scientists, it was not a question of *whether* to use race, but *how*, or more specifically *how much* (i.e., how fine-grained) race to use.

This debate took place while the NRC Committee was conducting its study of DNA technology in forensic science.[88] Its report, issued in 1992, discussed both sides of the issue without specifically taking sides. It did, however, choose "to assume for the sake of

---

[80] For a brief discussion of the conception of reification of race, see generally Duster, *supra* note 13, at 1050-51.

[81] Lewontin & Hartl, *supra* note 34, at 1747.

[82] *Id*. at 1749.

[83] *Id*. at 1747.

[84] Chakraborty & Kidd, *supra* note 72, at 1735.

[85] *Id.* at 1738.

[86] *Id.* at 1736-39.

[87] *Id*. at 1738-39.

[88] ARONSON, *supra* note 57, at 153-58.

discussion that population substructure may exist and to provide a method for estimating population frequencies in a manner that would adequately account for it."[89] The report recognized that "[p]opulation genetic studies show some substructure within racial groups for genetic variants. . . . Thus, North American Caucasians, [B]lacks, Hispanics, Asians, and Native Americans are not homogeneous groups."[90] In effect, this approach reflected the concerns expressed by Lewontin and Hartl, recognizing that social categories of race did not map neatly onto discrete, genetically definable population groups.

The NRC's 1992 report created problems for prosecutors. By taking cognizance of the difference of scientific opinion regarding the appropriate calculation of allele frequencies and RMPs, it seemed to assert that forensic DNA technologies lacked the sort of scientific consensus needed to support the introduction of such expert evidence.[91] Thus, for example, in the 1992 case of *People v. Barney*, the California Court of Appeal cited the NRC Report in concluding that disagreement and uncertainty in the scientific community regarding the selection of appropriate reference populations precluded the admission of DNA evidence based on the product rule.[92]

By April 1993, the director of the FBI asked the NAS to conduct a rapid follow-up study to resolve these uncertainties.[93] In 1994, the NRC formed a second committee (NRC II) with a specific mandate "to update and clarify discussion of the principles of population genetics and statistics as they apply to DNA evidence."[94] Meanwhile, the debate that continued concurrently in the scientific community would come to have significant consequences for the NRC II's subsequent report.

In 1994, Chakraborty and Kidd's position received a major boost. That year Eric Lander of Massachusetts Institute of Technology, previously a vigorous critic of the lack of adequate standards in DNA typing, paired with Bruce Budowle, one of the principal architects of the FBI's DNA-typing program, to write an article in the journal *Nature*, declaring "DNA fingerprinting dispute laid to rest."[95] The article argued that applying the product rule to the frequency estimates for four independent VNTRs generated odds of such magnitude that any technical statistical differences observed between the use of the broad racial databases (as advocated by Chakraborty and Kidd) versus more

---

[89] NRC I, *supra* note 39, at 12.

[90] *Id.* at 79.

[91] Kaye, *supra* note 26, at 102-03.

[92] *Id.* at 104 n.20.

[93] ARONSON, *supra* note 57, at 169.

[94] D.H. Kaye, *DNA, NAS, NRC, DAB, RFLP, PCR, and More: An Introduction to the Symposium on the 1996 NRC Report on Forensic DNA Evidence*, 37 JURIMETRICS 395, 397 (1997) (internal quotation marks and emphasis omitted).

[95] Eric S. Lander & Bruce Budowle, *DNA Fingerprinting Dispute Laid to Rest*, 371 NATURE 735, 735 (1994).

fine-grained ethnic subgroup databases (as advocated by Lewontin and Hartl) were "of no practical consequence to the courts."[96] As Lander and Budowle observed,

> In the vast majority of cases, a jury needs to know only that a particular DNA pattern is very rare to weigh it in the context of a case: *the distinction between frequencies of 10^{-4}, 10^{-6} and 10^{-8} is irrelevant in the case of suspects identified by other means*. . . . The most extreme positions range over a mere two orders of magnitude: whether the population frequency of a typical four-locus genotype should be stated, for example, as 10^{-5} or 10^{-7}. *The distinction is irrelevant for courtroom use.*[97]

Lander and Budowle were not arguing that racial subgroups themselves were not needed or desirable in calculating RMPs. The "distinction" they saw as "irrelevant" was the one between ethnic subgroups, such as Irish, and larger racial groups, such as Caucasian.[98] Thus, they were legitimating the then-current standard FBI practice of using broad racial groups such as "Black" and "Caucasian," as reference databases for generating allele frequencies for calculating RMPs.[99] Significantly, Lander and Budowle did not argue for doing away with racial databases altogether in favor of using an undifferentiated general population database. Given the current state of forensic technology, which generated RMPs from examining VNTRs at only four loci, they deemed race relevant.[100] They simply did not want too much of it—that is, they did not want law enforcement forced to undertake the burdensome task of developing more elaborate databases that reflected the wide array of genetic population substructuring that actually occurs across the globe.[101] Given the odds generated by testing at four VNTR loci, they deemed the broad racial categories of the Census more than adequate for forensic purposes.[102]

Lander and Budowle made a critical distinction between statistical and legal relevance. Though hardly the first to do so,[103] Lander and Budowle used the distinction to quiet both the scientific debates and the legal uncertainties swirling around this new and powerful forensic technology. This distinction continues to play a role throughout the continuing development and application of DNA technology up to present day cases such as *People v. Wilson*.[104] Another critic of the NRC's 1992 report, David Kaye, of the Arizona State University School

---

[96] *Id.* at 735; *see also id.* at 736.

[97] *Id.* at 738 (emphasis added).

[98] *Id.* at 736, 738.

[99] *Id.*

[100] *Id.* at 738.

[101] *Id.* at 737-38.

[102] *Id.*

[103] *See, e.g.*, Herman L. Trautman, *Logical or Legal Relevancy—A Conflict in Theory*, 5 VAND. L. REV. 385, 412 (1952).

[104] 136 P.3d 864, 865-66 (Cal. 2006).

of Law, made a similar distinction in a 1993 article in the *Harvard Journal of Law & Technology*.[105] Kaye, who sat on the second NRC Committee,[106] wrote that in calculating RMPs, "[t]he real issue . . . is not 'statistical significance' but rather practical or substantive significance."[107] The difference was critical for Kaye and others because it provided the basis for validating the then-current law enforcement practices of using broad racial reference population databases. By distinguishing between statistical versus logical or practical significance, Kaye and others, such as Lander and Budowle, did not refute Lewontin and Hartl so much as bracket off their concerns as irrelevant to the legal applications of forensic DNA technology in courts.[108] Of most immediate significance in terms of the unfolding story of the use of race in forensic DNA technology, is the fact that this distinction played a central role in the NRC II report, *The Evaluation of Forensic DNA Evidence*, issued in 1996.[109]

C. NRC II: Questions of Race Laid to Rest?

The NRC II report was undertaken to resolve the problems NRC I created for law enforcement by addressing "population genetics and statistics" related to the calculation of RMPs.[110] It "argue[d] for using separate databases for different racial groups"[111] even while it acknowledged Lewontin's underlying argument that "the variability among individuals within a population is greater than that between populations."[112] Recognizing the uncertainties inherent in calculating RMPs, the report noted that "[t]he accuracy of the estimate will depend on the genetic model, the actual allele frequencies, and the size of the database."[113] It was confident, however, that "when several loci are used, the probability of a coincidental match is very small."[114] Nonetheless, the report recommended incorporating a ten-fold margin of error in RMP calculation, stating, "If the calculated probability of a random match between the suspect and evidence DNA is 1/(100 million), we can say with confidence that the correct value is very likely between 1/(10 million) and 1/(billion)."[115]

---

105 Kaye, *supra* note 26, at 104.

106 NATIONAL RESEARCH COUNCIL, THE EVALUATION OF FORENSIC DNA EVIDENCE iii (1996) [hereinafter NRC II].

107 Kaye, *supra* note 26, at 126-27 (citation omitted).

108 *See* Lander & Budowle, *supra* note 95, at 736-38.

109 *See generally* NRC II, *supra* note 106.

110 Kaye, *supra* note 94, at 397 (quoting NRC II, *supra* note 106, at 1).

111 NRC II, *supra* note 106, at 21.

112 *Id.*

113 *Id.* at 33.

114 *Id.* at 34.

115 *Id.*

At first glance, such a range may strike the reader as rather large, but the report legitimizes it by returning to the distinction between statistical and legal relevance. According to the NRC II Report, the true issue

> is not whether the probability is large or small, but how accurate it is. Probabilities are not untrustworthy simply because they are small. In most cases, given comparable non-DNA evidence, a judge or jury would probably reach the same conclusion if the probability of a random match were one in 100,000 or one in 100 million.[116]

In other words, the large range presented earlier in the report was of little practical or legal significance so long as it was *good enough* to guide a judge or jury in their deliberations. It was good enough for two reasons: first, because it was *accurate*—accuracy here can be crucially distinguished from *precision*, which the large range of probabilities certainly lacks; second, because the lower end of the range still presented odds so vanishingly small as to render it indistinguishable from the upper end of the range *as a practical matter*—that is, the difference was deemed to be insufficient to have any practical effect on the conclusion a judge or jury would reach in using the evidence.

And yet, even accepting this huge range of variance, the report persisted in using race as an organizing category in calculating RMPs. Thus, even while acknowledging that "some assert that the word *race* is meaningless [in a genetic context,] . . . white (Caucasian), black (African American), Hispanic, east Asian (Oriental), and American Indian (Native American) [are] racial groups."[117] It justified this choice by asserting that "there are reproducible differences among the races in the frequencies of DNA profiles used in forensic settings, and these must be taken into account if errors are to be minimized."[118]

It is instructive to note here just where it is that "difference" made a difference in the calculation of RMPs. Difference was deemed insignificant when it manifested as a thousand-fold range for an "accurate" calculation using the product rule to compare a single sample against a single reference population database—that is, the "difference" between "one in 100,000 or one in 100 million" made no practical difference for use of the data in a court of law.[119] To be fair, as noted above, the NRC II report recommended calculating RMPs with a margin of error limited to ten-fold in either direction[120]—but this still translates into a variation of one hundred-fold between the lowest and highest estimate. But when race was at issue in the NRC II report, the

---

[116] *Id.* at 56.

[117] *Id.* at 57 (second emphasis omitted). The report noted that such grouping was "[f]or convenience, uniformity, and clarity." *Id.*

[118] *Id.* at 57-58.

[119] *Id.* at 56.

[120] *Id.* at 34.

"difference" of frequencies among racial reference populations became critical and had to be "taken into account if errors are to be minimized."[121]

Race enters into people's consciousness in complex and often unanticipated ways. The NRC II report clearly focused on issues of race in response to the questions raised by the debate in which Lewontin and Hartl opposed Chakraborty's and Kidd's views. That debate involved the relation between social groups of race and genetic variation.[122] Both sides recognized that racial categories were crude surrogates for capturing genetic variation across groups, but Chakraborty and Kidd were, in effect, arguing that race was nonetheless not "too crude"—that is, it was good enough for practical use in law enforcement because of the ability to generate astronomically low RMPs even allowing for a substantial range of variation.[123] As a practical matter, the debate cast into doubt the admissibility of DNA forensic evidence in courts; hence the FBI's urging that the issue be revisited by a second NRC Committee.[124] The NRC II report, therefore, aimed to quiet the dispute, rendering it irrelevant to the practical application of forensic DNA technologies in law enforcement. Yet, it is unclear why the NRC II report characterized difference among racial reference populations as meaningful "error," while it deemed the hundred (or even thousand) fold range of variance within a single reference population to be of no practical significance.[125] This seems largely to be an artifact of the report's focus on addressing the issues raised by Lewontin and Hartl in a manner that would allow forensic DNA testing to proceed unimpeded by concerns of the accuracy of using racial reference populations to calculate RMPs. The report needed to show that RMPs generated by using racial categories were good enough for practical use in courts of law. The utility and/or validity of using a general population database without reference to either race or ethnic subgroups was never really at issue.

In the end, the report issued the following formal recommendation for estimating RMPs:

> In general, the calculation of a profile frequency should be made with the product rule. If the race of the person who left the evidence-sample DNA is known, the database for the person's race should be used; if the race is not known, calculations for all the racial groups to which possible suspects belong should be made.[126]

The NRC II report thus legitimized the then standard practice of using race to generate RMPs. In rejecting Lewontin and Hartl's concerns

---

121 *Id.* at 57-58.
122 *See supra* text accompanying notes 62-87.
123 *See supra* text accompanying notes 84-87.
124 ARONSON, *supra* note 57, at 168-71.
125 *See* NRC II, *supra* note 106, at 56, 58-59.
126 *Id.* at 5.

about broad racial databases, it seems also, implicitly, to have rejected—or at least failed to fully appreciate—Lewontin's cognate concerns about the incoherence of race as a genetic category and the dangers of reifying race as genetic.[127]

III. CURRENT STANDARD PRACTICES REGARDING RACE AND FORENSIC DNA ANALYSIS

A. The Impact of NRC II

The NRC II report became tremendously influential in shaping forensic DNA techniques and their acceptance in courts of law. It established new norms for calculating RMPs generally and for using race-specific databases in particular. Following the NRC II recommendation, it has since become standard practice to present race-specific RMPs.[128] Thus, for example, in the 1999 case of *People v. Soto*,[129] the California Supreme Court noted that the dispute regarding population substructuring, which had been at the heart of the 1992 case of *People v. Barney*,[130] had "been eclipsed by subsequent important scientific developments, most notably the publication in 1996 of a completely new report by the NRC . . . ."[131] The court concluded that using the product rule with respect to broad racial databases "has gained general acceptance in the relevant scientific community."[132] Similarly, in *People v. Wilson*,[133] the court referenced testimony by the California Department of Justice's criminologist, Nicola Shea, in stating that "to help juries understand the significance of a DNA match, the Department followed the statistical approach recommended by [the NRC II report] for presenting the frequency with which genetic profiles occur."[134]

In cases such as *Soto* and *Wilson* we see that the use of racial databases characterized by the broad terms of the U.S. Census categories had emerged as normative referents for the calculation of RMPs. Thus, for example, in justifying its calculation of RMPs in *Wilson*, the State of California argued that the lower court

> correctly approve[d] the California Department of Justice's (DOJ) *generally accepted* method for generating match probability statistics using reference data from major racial and ethnic groups. *Typically*, a range of statistics is

---

127 *See, e.g.*, Lewontin, *supra* note 66, at 381-83.

128 *See, e.g.*, BUTLER, *supra* note 3, at 474-517.

129 981 P.2d 958 (Cal. 1999).

130 10 Cal. Rptr. 2d 731, 743 (Ct. App. 1992).

131 *Soto*, 981 P.2d at 960. Further in the case the court notes that developments since *Barney* included an FBI world study of genetic variation in 1993, the publication of the article in NATURE by Lander and Budowle, and, "of greatest significance," the NRC II report. *Id.* at 975-76.

132 *Id.* at 960.

133 136 P.3d 864 (Cal. 2006).

134 *Id.* at 866.

> provided using three major U.S. population databases: African-American, Caucasian, and Hispanic. This method . . . is supported by *NRC II*.[135]

As representative of current practice, *People v. Wilson* shows how fully integrated race has become in the conceptualization and practice of forensic DNA analysis. The use of race by the State is understood as requiring no justification other than that it had become "generally accepted" and is "typical."

B. CODIS and the Move from VNTRs to STRs

The NRC II report itself was based largely on an assessment of the then-current practice of testing samples at four VNTR loci.[136] Ironically, by 1997, barely a year after the report had issued, a new technology had emerged to replace four loci VNTR analysis using restriction fragment polymorphism (RFLP) methods of analysis.[137] In 1985 Kary Mullis, along with a research group at the Cetus Corporation, discovered a technique known as Polymerase Chain Reaction (PCR), which enabled scientists "to make millions of copies of a specific sequence of DNA in a matter of only a few hours."[138] The ability to amplify segments of DNA is critical to forensic analysis.[139] The benefits of PCR are that it "is sensitive, rapid, and not limited by the quantity of DNA as . . . [RFLP] methods are."[140] PCR enabled a shift in focus from VNTRs to sections of DNA known as "Short Tandem Repeats" (STRs).[141] VNTRs are typically ten to one hundred bases in length.[142] STRs (also known as microsatellites) are regions of DNA only two to six base pairs in length.[143] STRs are highly variable across individuals and are easily amplified by PCR, thus making them very effective for purposes of human identification.[144]

In 1996, the FBI commenced an effort to develop a set of STR loci to be used as standard referents for the calculations of RMPs in forensic DNA analysis.[145] In November 1997, the FBI settled on thirteen core STR loci to be the basis of the CODIS (COmbined DNA Index

---

[135] Answer Brief on the Merits at 2-3, People v. Wilson, 136 P.3d 864 (Cal. 2006) (No. S130157) (emphasis added).

[136] NRC II, *supra* note 106, at 65-74.

[137] BUTLER, *supra* note 3, at 94.

[138] *Id.* at 63; *see also* Randall K. Saiki, *Enzymatic Amplification of Beta-Globin Genomic Sequences and Restriction Site Analysis for Diagnosis of Sickle Cell Anemia*, 230 SCIENCE 1350 (1985).

[139] BUTLER, *supra* note 3, at 63.

[140] *Id.*

[141] *Id.* at 85.

[142] *Id.*.

[143] *Id.*

[144] *Id.*

[145] *Id.* at 94.

System) national DNA Database, which was launched in 1998.[146] New technologies allowing for "multiplex" testing of multiple loci at once were soon capable of regularly generating RMPs rarer than one in one trillion.[147] The Minnesota State Department of Public Safety has noted that "STRs are very discriminating for single-source samples. Typically, a complete DNA profile might be found in less than one in one hundred billion people. A typical DNA report would read 'This profile would not be expected to occur more than once among unrelated individuals in the world population.'"[148] By 2000 the FBI laboratory and many others stopped using RFLP analysis altogether in favor of PCR analysis of the thirteen CODIS STRs.[149] Because of their use in the FBI database, the thirteen CODIS STRs have become a national (indeed international) standard and have come to "dominate the genetic information that has been collected to date on human beings."[150]

CODIS was initially authorized by the DNA Identification Act of 1994[151] and became operational in 1998.[152] As described by the FBI,

> CODIS is implemented as a distributed database with three hierarchical levels (or tiers)—local, state, and national. NDIS [National DNA Index System] is the highest level in the CODIS hierarchy, and enables the laboratories participating in the CODIS Program to exchange and compare DNA profiles on a national level. All DNA profiles originate at the local level (LDIS), then flow to the state (SDIS) and national levels. SDIS allows laboratories within states to exchange DNA profiles. The tiered approach allows state and local agencies to operate their databases according to their specific legislative or legal requirements.[153]

As of October 2007, there were over five million DNA profiles in CODIS.[154] The profiles themselves are not classified by race. Rather they are primarily used, much like a database of fingerprints, to aid in the investigation of crimes by providing matches or "hits" to DNA evidence left at crime scenes.[155] In the context of establishing an initial match using the CODIS database, race is therefore irrelevant.

---

[146] *Id.* at 13, 94.

[147] *Id.* at 94-95; Budowle et al., *supra* note 17.

[148] Bureau of Criminal Apprehension Forensic Sci. Lab., Minn. Dep't of Pub. Safety, Guide to DNA Analysis 2 (Mar. 2003), http://www.bca.state.mn.us/Lab/Documents/DNAbroc03.pdf.

[149] BUTLER, *supra* note 3, at 13.

[150] John M. Butler, *Genetics and Genomics of Core Short Tandem Repeat Loci Used in Human Identity Testing*, 51 J. FORENSIC SCI. 253, 253 (2006).

[151] DNA Identification Act of 1994, 42 U.S.C. § 14131 (1994).

[152] *See* Fed. Bureau of Investigation, The FBI's Combined DNA Index System Program: CODIS (Apr. 2000), http://www.dna.gov/rawmedia_repository/7d77e285_f2c0_4098_8863_fe744ce72e3b.

[153] *Id.*; *see also* Maclin, *supra* note 47, at 166.

[154] National DNA Index System, http://www.fbi.gov/hq/lab/codis/national.htm (last visited Aug. 23, 2008).

[155] BUTLER, *supra* note 3, at 439. DNA databases are also used to aid investigations in identifying human remains. *Id.* at 443.

Nonetheless, race has come to pervade the characterization of forensic DNA data generated using the standard thirteen CODIS loci. This is because establishing a match is only the first step in applying forensic DNA technology.[156] Once a match is found, whether using the CODIS database or not, law enforcement must still take the further step of calculating an RMP for any given DNA profile.[157] It is at this stage that race enters CODIS—and in a more powerful way than ever before. In addition to the basic CODIS database, the FBI has generated a population file to estimate allele frequencies according to specifically identified racial or ethnic groups.[158] This population file is based on a 2001 study led by Bruce Budowle, which typed allele frequencies for the thirteen CODIS loci from forty-one population data sets.[159] Budowle classified the results in terms of five "major population groups: African American, U.S. Caucasian, Hispanic, Far East Asian, and Native American."[160] These allele frequencies have since become the standard reference database for calculating racially identified RMPs.[161] Thus, for example, in *People v. Wilson*, the court, referencing the Budowle study, noted that criminologist Nicola Shea described how the Department of Justice "used databases that the Federal Bureau of Investigation published in the Journal of Forensic Sciences reflecting profile frequencies in the Caucasian, Hispanic and African-American populations."[162]

IV. RACE, TECHNOLOGY, AND "CARE OF THE DATA"[163]

A. Race Versus Technology

The casual and perfunctory assignment of social categories of race to biological samples in professional discussions of forensic DNA stands in marked contrast to the meticulous care taken concerning the more technical aspects of DNA extraction, amplification, and analysis. The discussions of each in a 2005 article[164] by Peter Vallone, Amy

---

156 *See supra* text accompanying notes 26-27.

157 *Id.*

158 BUTLER, *supra* note 3, at 439.

159 Bruce Budowle et al., *CODIS STR Loci Data from 41 Sample Populations*, 46 J. FORENSIC SCI. 453, 453 (2001) [hereinafter Budowle, *CODIS STR Loci Data*].

160 *Id.*

161 *See* BUTLER, *supra* note 3, at 439.

162 People v. Wilson, 136 P.3d 864, 866 (Cal. 2006).

163 For an elaboration of the concept of "care for the data," see Kim Fortun & Mike Fortun, *Scientific Imaginaries and Ethical Plateaus in Contemporary U.S. Toxicology*, 107 AM. ANTHROPOLOGIST 43, 49-50 (2005).

164 Peter M. Vallone et al., *Allele Frequencies for 70 Autosomal SNP Loci with U.S. Caucasian, African-American, and Hispanic Samples*, 149 FORENSIC SCI. INT'L 279 (2005). Other similar treatments of both race and technique in forensic DNA analysis can be found in John M. Butler et al., *Allele Frequencies for 15 Autosomal STR Loci on U.S. Caucasian, African American, and Hispanic Populations*, 48 J. FORENSIC SCI. 4 (2003); Budowle, *CODIS STR Loci Data*, *supra*

Decker, and John Butler, of the National Institute of Standards and Technology's (NIST) Human Identity Project[165] team, are fairly typical. This particular article involved the characterization of allelic frequencies for seventy single nucleotide polymorphisms ("SNPs") in DNA samples taken from three racially marked groups: U.S. Caucasian, African-American, and Hispanic.[166] The article presents its techniques for racially identifying the DNA samples as follows: "Anonymous liquid blood samples with self-identified ethnicities were purchased from Interstate Blood Bank, Inc. (Memphis, TN) and Millennium Biotech, Inc. (Ft. Lauderdale, FL)."[167] "Self-identification" thus provides the sum total of all care and technique devoted by Vallone et al. to characterizing genetic samples by race. Contrast this with their discussion of the more apparently technical aspects of how they manipulated the samples once in the lab (which is quoted at length to heighten the contrast):

> 2. DNA extraction
> Blood samples were extracted using a modified salting out procedure.
>
> 3. Quantification
> Extracted DNA was quantified using UV spectrophotometry followed by a PicoGreen assay to adjust concentrations to approximately 1 ng/µl.
>
> 4. SNP markers
> The 70 autosomal SNP markers are listed in Table 1 (see also http://www.cstl.nist.gov/biotech/strbase/SNP.htm). The PCR primer sequences were obtained from Orchid Cellmark (personal communication, Jeanine Baisch, Orchid Cellmark Dallas). The exact chromosomal locations were ascertained using BLAT (http://genome.ucsc.edu/cgi-bin/hgBlat) and dbSNP (http://www.ncbi.nlm.nih.gov/SNP/) and are based on the July 2003 assembly of the human genome. All of the SNPs are C/T transitions.
>
> 5. PCR amplification
> For each sample, the 70 SNP markers were typed in 11 unique 6-plexes and a single 4-plex PCR. The final concentrations of the six (or 4) PCR primer pairs were present at 0.5 µM for all multiplex PCRs. Amplifications were performed in reaction volumes of 10 µl using a master mix containing 1X GeneAmp® PCR Gold buffer (Applied Biosystems, Foster City, CA), 4.5 mmol/l $MgCl_2$, 250 µmol/l deoxynucleotide triphosphates (dNTPs; Promega Corporation, Madison, WI), 0.16 mg/ml bovine serum albumin (BSA) fraction V (Sigma, St. Louis, MO), and 0.5 unit of AmpliTaq Gold® DNA polymerase (Applied Biosystems). The thermal cycling program was carried out on a GeneAmp 9700 (Applied Biosystems) using the following conditions in 9600-emulation mode (i.e., ramp speeds of 1 °C/s):

---

note 159, at 453; Bruce Budowle & Tamyra R. Moretti, *Genotype Profiles for Six Population Groups at the 13 CODIS Short Tandem Repeat Core Loci and Other PCR-Based Loci*, 1 FORENSIC SCI. COMM. 2 (1999), *available at* http://www.fbi.gov/hq/lab/fsc/backissu/july1999/budowle.htm.

[165] The Human Identity Project at the NIST is funded by the National Institute of Justice to improve forensic DNA testing methods. National Institute of Standards and Technology, DNA Measurements, http://www.cstl.nist.gov/div831/DNATechologies/Human_Identity.htm (last visited Aug. 20, 2008).

[166] Vallone et al., *supra* note 164, at 279.

[167] *Id.*

> 95 °C for 10 min
> Three cycles of {95 °C for 30 s, 50 °C for 55 s, 72 °C for 30 s}
> 18 cycles of {95 °C for 30 s, 50 °C for 30 s +0.2 °C per cycle.
> 72 °C for 30 s}
> 11 cycles of {95 °C for 30 s, 55 °C for 30 s, 72 °C for 30 s}
> 72 °C for 7 min
> 25 °C until removed from thermocycler
>
> Following PCR amplification, unincorporated primers and dNTPs were removed by adding 4 µl of a Exo-SAP enzyme cocktail consisting of 1.4 µl Exonuclease I (10 U/µl) and 2.6 µl (1U/µl) of shrimp alkaline phosphatase (SAP; USB Corp., Cleveland, OH) to each 10 µl PCR reaction. Reactions were mixed briefly and incubated at 37 °C for 90 min and then 80 °C for 20 min to inactivate the enzymes.[168]

The point here is not to assess (or even understand) the intricacies of the technical analysis performed by Vallone et al. on their DNA samples. Rather, it is to contrast the extreme care and detail devoted to illustrating the techniques performed in the lab with the casual and perfunctory discussion of how the samples came to be racially marked in the first place. As scientists, Vallone et al. understandably go into greatest detail with respect to those very techniques and practices in which they are professionally trained and proficient. This detail reflects their reasonable understanding that the extraction, amplification, and analysis of DNA take great care and expertise.

The contrasting lack of care taken in characterizing the racial identity of the genetic samples indicates an implicit assumption that such characterizations are obvious, uncomplicated, and take no special expertise. This contrast may be understood more broadly as reflecting a conceptual separation of the world of the "social" from that of the "natural," where the former is understood to contain transparent categories accessible to all, while the latter requires specialized knowledge and expertise for proper analysis and interpretation. In other words, race is seen as easy and obvious; DNA is seen as difficult and complex.[169] There is an utter failure to consider that social subjects such as race may demand similar rigor, expertise, and care in handling as scientific subjects such as DNA.

---

[168] Peter M. Vallone et al., *Allele Frequencies for 70 Autosomal SNP Loci with U.S. Caucasian, African-American, and Hispanic Samples*, 149 FORENSIC SCI. INT'L 279, 279-80 (2005).

[169] This lack of comparable care is not restricted to the arena of forensics. For example, a recent survey of biomedical studies using race as a variable found that 72% of 268 reports analyzed did not explain their methods of assigning race or ethnicity as independent variables. Hasan Shanawani et al., *Non-reporting and Inconsistent Reporting of Race and Ethnicity in Articles that Claim Associations among Genotype, Outcome, and Race or Ethnicity*, 32 J. MED. ETHICS 724, 724-25 (2006).

B. Social Versus Genetic "Race"

Ironically, this separation of the social from the natural is enabled by the work of geneticists such as Lewontin who, together with a wide array of social scientists, have worked diligently since World War II to reconfigure race from a biological construct into a social construct.[170] It is precisely because race is currently widely understood as a social phenomenon that forensic scientists are able to effectively marginalize it from their analysis of the biological construct of DNA. As a result, their care of the data extends only to the analysis of DNA samples while wholly overlooking the complexities of using racial categories in relation to genetics.

In effect, forensic scientists have simply adopted the broad categories of race and ethnicity used in the U.S. Census to organize their genetic data.[171] The Census, in turn, is based on the Office of Management and Budget's ("OMB") Directive 15 on "Race and Ethnic Standards for Federal Statistics and Administrative Reporting,"[172] which provides the following categories as a minimum standard for maintaining, collecting, and presenting data on race and ethnicity for all federal reporting purposes: American Indian or Alaska Native; Asian; Black or African American; Hispanic or Latino; Native Hawaiian or Other Pacific Islander; and White.[173]

These federally mandated standards emerged as a consequence of major government programs and legal initiatives instituted since the 1960s. The OMB categories provide the basis for both census information and access to a variety of governmental goods and services that are contingent upon membership in a particular racial or ethnic group.[174] For example, federal users of racial data provided by the census include: the Department of Education, Department of Justice, Department of Labor, Equal Employment Opportunity Commission, Federal Reserve, Department of Health and Human Services, Housing and Urban Development, Department of Agriculture, and the Veterans

---

[170] *See generally* Lewontin, *supra* note 66. For an excellent overview of the history of scientific and cultural understandings of race, see generally JONATHAN MARKS, HUMAN BIODIVERSITY: GENES, RACE, AND HISTORY (1995). For some influential statements on race by professional social science organizations, see, e.g., American Anthropological Association, Response to OMB Directive 15: Race and Ethnic Standards for Federal Statistics and Administrative Reporting (Sept. 1997), http://www.aaanet.org/gvt/ombdraft.htm; American Anthropological Association, Statement on "Race" (May 17, 1998), http://www.aaanet.org/stmts/racepp.htm; American Sociological Association, The Importance of Collecting Data and Doing Social Scientific Research on Race (2003), http://asanet.org/galleries/default-file/asa_race_statement.pdf.

[171] *Forensic Genetics*, *supra* note 13, at S9. Most influential in this regard is a foundational article by Budowle. *See generally* Budowle, *CODIS STR Loci Data*, *supra* note 159.

[172] Revisions to the Standards for the Classification of Federal Data on Race and Ethnicity, 62 Fed. Reg. 58,782, 58,782 (Oct. 30, 1997), *available at* http://www.whitehouse.gov/omb/fedreg/ombdir15.html.

[173] *Id.* at 58,788-89; *see also* Racial and Ethnic Classifications, *supra* note 1.

[174] MELISSA NOBLES, SHADES OF CITIZENSHIP: RACE AND THE CENSUS IN MODERN POLITICS 75-79 (2000).

Administration.[175] Alice Robbin notes that "[g]roups must be counted in order to make credible claims for political representation, demonstrate discriminatory practices against them, seek and obtain legal remedies, receive governmental assistance for a host of social programs, and evaluate current, as well as develop new public policy."[176] Additionally, the OMB racial and ethnic categories provide the framework for evaluating school desegregation, electoral districting, and other civil rights initiatives.[177]

Given the social and political uses which such standards were designed to serve, it should come as no surprise that Directive 15 explicitly acknowledges that the categories it provides are social in character, not biological or genetic.[178] Using these same categories in the context of genetic research, however, presents issues of a different order. As Lee et al. note,

> [r]esearch utilizing race serves to "naturalize" the boundaries dividing human populations, making it appear that the differences found reflect laws of nature. In fact, the use of race and ethnicity in biomedical research is problematic because it is caught in a tautology, both informed by, and reproducing, "racialized truths."[179]

This dynamic reinforces what sociologist Michael Omi has characterized as "an interesting dilemma facing scientists in the United States. On one hand," Omi asserts, "scientists routinely use racial categories in their research . . . . On the other hand, many scientists feel that racial classifications are meaningless and unscientific."[180]

C. The Obvious Solution: A Non-Racial, General Population Database

Race was originally introduced into the calculation of RMPs in the early years of forensic DNA analysis in the hope of providing more refined statistical calculations.[181] The rationale was grounded in the reasonable observation that there is a modicum of genetic variation across certain human populations.[182] Capturing this variation might

---

[175] Racial and Ethnic Classifications, *supra* note 1; *see generally* Alice Robbin, *The Politics of Representation in the US National Statistical System: Origins of Minority Population Interest Group Participation*, 27 J. GOV'T INFO. 431 (2000).

[176] Robbin, *supra* note 175, at 435.

[177] *See generally* Michael Omi, *Racial Identity and the State: The Dilemmas of Classification*, 15 LAW & INEQ. 7 (1997); Alice Robbin, *Classifying Racial and Ethnic Group Data in the United States: The Politics of Negotiation and Accommodation*, 27 J. GOV'T INFO. 129, 148-50 (2000).

[178] Revisions to the Standards for the Classification of Federal Data on Race and Ethnicity, 62 Fed. Reg. at 58,782, 58,788.

[179] Lee et al., *supra* note 13, at 55 (footnote omitted) (citation omitted).

[180] Omi, *supra* note 177, at 7.

[181] *See supra* text accompanying notes 52-97.

[182] *See supra* text accompanying notes 52-97.

provide more accurate RMPs.[183] Greater accuracy was important in the early years of forensic DNA analysis when RMPs were generated using only four VNTR loci.[184] With such limited data, the variation of RMPs generated using different reference populations could be of forensic significance.[185]

Today the situation has changed significantly. With the advent of multiplex assays testing for the thirteen standard CODIS loci, forensic scientists are now capable of regularly generating RMPs with denominators many times in excess of the entire world's population.[186] As another article with the FBI's Bruce Budowle as lead author put it, as early as 2000, "[b]y typing these [13] STR loci, the random match probability for a multiple locus profile will be exceedingly small. The average random match probability for unrelated individuals for the 13 STR loci is less than one in a trillion, even in populations with reduced genetic variability."[187] Under such circumstances, the concern originally expressed by Lewontin and Hartl—that using broader racial categories will not produce accurate enough RMPs—fades into irrelevance.[188] As a practical matter, when one is dealing with odds in the hundreds of billions or trillions, the more fine-grained characterizations of genetic variation among ethnic subgroups called for in Lewontin and Hartl's 1991 *Science* article[189] are simply not necessary.

The issue then shifts from *how much* race to use to *whether* to use race at all. As is made evident by the range of odds generated in cases such as *People v. Wilson* ("one of 96 billion Caucasians, one of 180 billion Hispanics, and one of 340 billion African-Americans"),[190] the use of a non-racially marked general reference population would still generate RMPs whose reciprocals would exceed the world's population many fold. Under such circumstances, any differences between RMPs generated by using race-specific reference populations and a general population are without forensic significance. Thus, it is no longer necessary even to use the broad racial reference populations advocated by Chakraborty and Kidd back in 1991.[191]

The possibility of abandoning racial reference populations in favor of a general population database was broached in a 2000 report by the National Institute of Justice's National Commission on the Future of DNA Evidence.[192] In the context of discussing the rise of testing for

---

183 *See supra* text accompanying notes 52-97.
184 *See supra* text accompanying notes 124-131.
185 *See supra* text accompanying notes 124-131.
186 Budowle et al., *supra* note 17.
187 *Id.* (internal citations omitted).
188 Lewontin & Hartl, *supra* note 34, at 1746.
189 *Id.* at 1749-50.
190 People v. Wilson, 136 P.3d 864, 867 (Cal. 2006).
191 Chakraborty & Kidd, *supra* note 72, at 1738-39.
192 FUTURE, *supra* note 33.

STRs in contrast with the older method of VNTR analysis, the report noted that

> [i]t is already apparent that most of the STR variability is within groups. Although groups differ, the mean differences between groups are less than the individual differences within groups; profiles that are rare in one group tend to be rare in others. *With enough loci it may be possible to have a single database for all the major groups in the United States.*[193]

Given the ability to generate RMPs in the trillions, it seems obvious that we currently have enough loci to have a single non-racial reference population database. The question remains, "Why do we continue to use race?"

D. The Inertial Power of Race

There is no easy answer to this question. I suggest that there is an inertial power to race in American society that propels the continued use of race long after any original rationale for its introduction may have faded. In particular, I consider three possible dynamics contributing to the persistent use of race in the presentation of forensic DNA evidence even after current technology has obviated the need for race-specific databases: 1) the persistent conceptualization of race as genetic; 2) the confusion of statistical significance with forensic significance; and 3) the deep-seated American identification of violent crime and race.

First, with respect to genetics, in spite of decades of efforts on the part of social and natural scientists to sever the ties between race and biology, large segments of American society continue to conceptualize race primarily in genetic terms.[194] The rise of modern genomics was supposed to resolve the dispute.[195] Upon the completion of the first draft of the human genome in 2000, President Clinton declared, "After all, I believe one of the great truths to emerge from this triumphant expedition inside the human genome is that in genetic terms all human beings, regardless of race, are more than 99.9% the same."[196]

At the same press conference, Dr. J. Craig Venter, president and CEO of Celera Genomics, reinforced Clinton's message, asserting that "the concept of race has no genetic or scientific basis."[197] Yet, ironically, since this iconic press conference, genetic conceptualizations of race seem to have reemerged with a vengeance. As anthropologist Sandra Lee has noted,

---

[193] *Id.* at 27 (emphasis added).

[194] Sandra Soo-Jin Lee, *Biobanks of a "Racial Kind": Mining for Difference in the New Genetics*, 40 PATTERNS OF PREJUDICE 443, 447-48 (2006).

[195] *Id.*

[196] *Reading the Book of Life: White House Remarks on Decoding of Genome*, N.Y. TIMES, June 27, 2000, at F8.

[197] *Id.*

> the current trajectory of genomic research is increasingly focused on the 0.01 per cent genetic difference that is believed to separate one individual from another. The search for functional genetic variability is increasingly taken up in populations that are identified by conventional notions of race. This trajectory is the result of a confluence of factors, including a growing infrastructure of research materials that are racially categorized through the creation of biobanks. Such sorting practices reflect the ongoing conflict over the meaning of 'race' in science and medicine. In the emerging era of the new genetics, in which super-computer technology has given way to an explosion of human genetic data, biobanks that utilize taxonomies of race in the classification, storage and distribution of DNA samples become racializing technologies that promote notions of racial biology in research protocols designed to discover group difference.[198]

Sociologist Troy Duster has further argued that "new claims that DNA analysis of crime scene data will assist criminal investigations" have led to a "molecular reinscription of race in the biological sciences."[199] The same technology underlying the creation of racialized forensic DNA databases is also being used for drug development[200] and to market new genetic ancestry tracing services.[201] Thus, there have emerged both structural and commercial incentives to continue to use race in relation to genetics. This dynamic undergirds the inertial power of race in forensic DNA analysis by providing a broader context in which race is understood, somehow, to be naturally or logically connected to genetics. This dynamic is further reinforced by the tendency of forensic DNA experts, as discussed above,[202] to take race as an obvious, unproblematic category that does not require the same care and analysis as genetic data.

Second, the technical ability to generate statistically significant variation in RMPs across racial databases has led to the unquestioned assumption that such variation is also legally significant. Using the thirteen CODIS loci, forensic experts around the world have characterized allele frequencies for numerous ethnically and racially marked populations.[203] Modest frequency variation at each individual locus, when multiplied across loci by the product rule, can lead to apparently significant variations in RMPs across races.[204] Thus, in cases

---

[198] Lee, *supra* note 194, at 448-49 (internal quotation marks omitted).

[199] Troy Duster, *The Molecular Reinscription of Race: Unanticipated Issues in Biotechnology and Forensic Science*, 40 PATTERNS OF PREJUDICE 427, 427 (2006).

[200] *See, e.g.*, Jonathan Kahn, *From Disparity to Difference: How Race-Specific Medicines May Undermine Policies to Address Inequalities in Health Care*, 15 S. CAL. INTERDISC. L.J. 105, 105-06 (2005) [hereinafter Kahn, *Disparity*]; Jonathan Kahn, *Race-ing Patents/Patenting Race: An Emerging Political Geography of Intellectual Property in Biotechnology*, 92 IOWA L. REV. 353, 355 (2007).

[201] Deborah A. Bolnick et al., *The Science and Business of Genetic Ancestry Testing*, 318 SCIENCE 399, 399-400 (2007).

[202] *See supra* Part IV.A.

[203] *See, e.g.*, National Institute of Standards and Technology, *Population Survey*, http://www.cstl.nist.gov/strbase/population/PopSurvey.htm (last visited Nov. 21, 2008).

[204] Lempert, *supra* note 41, at 6-7.

such as *People v. Wilson*, the variation in RMPs across race-specific databases may appear, at first blush, to be important.[205] In that case, RMPs varied from 1 in 96 billion Caucasians, to 1 in 180 billion Hispanics, and 1 in 340 billion African-Americans.[206] According to the databases, defendant Wilson's genetic profile was more the three times as likely to occur in a Caucasian as an African-American—an apparently significant difference. But in the forensic context, this statistically significant difference has no real practical importance. When the world's population is under seven billion, the difference between an RMP of 1 in 96 billion and an RMP of 1 in 340 billion provides no meaningful distinction for a finder of fact. Both are astronomically low probabilities. Nonetheless, experts' ability to generate statistically significant differences across races seems to have propelled the continued use of racial databases—even when these differences are of no practical legal significance.[207]

Ironically, the reverse logic is used by law enforcement to support the rising use of race to generate suspect profiles from DNA evidence left at the scene of a crime.[208] This sort of genetic racial profiling uses allele frequencies to generate an estimate of the likely racial or ethnic background of an as yet unidentified perpetrator.[209] In this context, Troy Duster notes that law enforcement officials themselves have made a distinction between theoretical and practical significance of racial difference in genetics. Thus, as Duster notes,

> [w]hen representative spokespersons from the biological sciences say that there is no such thing as race, they mean, correctly, that there are no discrete racial categories that come to a discrete beginning and end, that there is nothing mutually exclusive about our current (or past) categories of race, and that there is more genetic variation within categories of race than between them. All this is true. However, when Scotland Yard or the Birmingham police force or the New York Police Department wants to narrow the list of suspects in a crime, they are not primarily concerned with tight taxonomic systems of classification with no overlapping categories. That is the stuff of theoretical physics and philosophical logic, not the practical stuff of crime-solving or the practical application of molecular genetics for health delivery via genetic screening, and all the messy overlapping categories that will inevitably be involved with such enterprises. That is, some African Americans have cystic fibrosis even though the likelihood of that is far greater among Americans of North European descent and, in a parallel if not symmetrical way, some American Whites have sickle cell anaemia even though the likelihood of that is far greater among Americans of West African descent. But in the world of cost-effective decision-making, genetic screening for these disorders is routinely based on

---

[205] People v. Wilson, 136 P.3d 864, 865-66 (Cal. 2006).

[206] *Id.* at 867.

[207] For further discussion of the difference between legal and statistical significance, see *supra* notes 156-157, 166 and accompanying text.

[208] Duster, *supra* note 199, at 434-35.

[209] *See supra* note 13.

> commonsense versions of the phenotype. The same is true with regard to the quite practical matter of naming suspects.[210]

Here, the scientific understanding that race is not genetic is trumped in practice by the purported ability of some genetic tests to estimate the likelihood that a suspect belongs to one or another socially identifiable race. Law enforcement is using race because it is perceived to be of practical significance—even if not scientific.[211] Yet, in the courtroom context, it appears that the reverse is the case: race is used because it is perceived as scientific—even if not of practical significance.

Race persists largely because it has become normative; an unquestioned, standardized practice that persists long after the rationale for it has faded. In *Wilson*, the State argued for the legitimacy of using race-specific RMPs on the grounds that such was the "standard practice"[212] and the "generally accepted method for generating match probability statistics"[213] and that "typically" the state and federal labs used "three major U.S. population databases: African-American, Caucasian, and Hispanic."[214] General acceptance, typicality, and standardization—these all powerfully drive the inertial power of race.

Third, there is the unfortunate but well documented tendency in the United States to identify race and violent crime. In *Whitewashing Race*, Michael Brown et al. discuss a cultural shift that began in the 1960s when the image of "the brave little girl walking up to the schoolhouse door in the face of jeering white crowds was replaced by fearsome young black men coming down the street ready to take your wallet or your life."[215] In the context of the rising racialization of crime in the United States, Rothenberg and Wang observe that "[f]rom 1990 to 2004, blacks were five times more likely than whites to be incarcerated, and in 2000, blacks and Latinos comprised 63% of incarcerated adults, even though together they represented only 25% of the total population."[216] Similarly, while examining the impact of DNA technology on the criminal justice system, Simon Cole concludes that

> [a]t the endpoint of this system is a carceral system that embodies gross race and class disparities, even if differential rates of offending are taken into account: two thirds of people in prison are racial and ethnic minorities, one in

---

[210] Duster, *supra* note 199, at 435 (internal quotation marks omitted).

[211] *Id.*

[212] People v. Wilson, 136 P.3d 864, 868 (Cal. 2006).

[213] Answer Brief on the Merits at 2, People v. Wilson, 136 P.3d 864 (Cal. 2006) (No. S130157).

[214] *Id.*

[215] MICHAEL K. BROWN ET AL., WHITEWASHING RACE: THE MYTH OF A COLOR-BLIND SOCIETY 132 (2003).

[216] Karen Rothenberg & Alice Wang, *The Scarlet Gene: Behavioral Genetics, Criminal Law, and Racial and Ethnic Stigma*, LAW & CONTEMP. PROBS., Winter/Spring 2006, at 343, 352.

> eight black males in their twenties are in prison or jail, three-quarters of persons in prison for drugs are people of color.[217]

Considering the dynamics that have produced such inequalities, Brown et al. review an array of historical, legal, and sociological data on race and crime in the United States. Citing a "classic . . . observational study of police responses to juveniles in a midwestern city in the 1960s,"[218] they note that police "'justified their selective treatment' [of black youths] on 'epidemiological lines,'" concentrating on "'those youths whom they believed were most likely to commit delinquent acts.'"[219] They argue, however, that

> the result of this "actuarial" reasoning . . . is to exacerbate the very differences that are invoked to justify the racially targeted practices in the first place. This in turn helps to cement the public's image, and the police's image, of the gun-toting gangster or drug dealer as black or Latino. And this confirms the validity of the police focus on youth of color, which then goes around and around in the same kind of vicious circle . . . described a generation ago.[220]

The same sort of actuarial reasoning is at work in Duster's identification of the use of genetics in the "practical matter of naming suspects."[221] The association of crime and race produces more racialized crime.[222] As Dorothy Roberts has noted, the resulting mass incarceration is "iatrogenic"[223]—by damaging social networks, distorting social norms, and destroying social citizenship, the disproportionate incarceration of minorities has produced a vicious cycle of crime and repression that further reinforces the identification of race and crime in the public mind.[224]

Taken together, the persistent conceptualization of race as genetic, the confusion of statistical with forensic significance, and the deep-seated American identification of violent crime and race may be understood to frame and facilitate the inertial power of race—to perpetuate itself as a salient category of forensic DNA analysis long after its practical legal utility has passed.

---

[217] Simon A. Cole, *How Much Justice Can Technology Afford? The Impact of DNA Technology on Equal Criminal Justice*, 34 SCI. & PUB. POL'Y 95, 98 (2007).

[218] BROWN ET AL., *supra* note 215, at 149.

[219] *Id.* at 150 (quoting Irving Piliavin & Scott Briar, *Police Encounters with Juveniles*, 70 AM. J. OF SOCIOLOGY 206, 212 (1964)).

[220] *Id.* at 151.

[221] Duster, *supra* note 199, at 435.

[222] Dorothy E. Roberts, *The Social and Moral Cost of Mass Incarceration in African American Communities*, 56 STAN. L. REV. 1271, 1297 (2004).

[223] *Id.*

[224] *See id.*; *see also generally* Rose M. Brewer & Nancy A. Heitzeg, *The Racialization of Crime and Punishment*, 51 AM. BEHAV. SCIENTIST 625 (2008) (arguing that the recent explosion in criminalization and incarceration is unprecedented in size, scope, and negative consequences—both direct and collateral—for communities of color).

V. PRESENTING RACE AND FORENSIC DNA IN COURT

In discussing the possibility of moving beyond race in forensic DNA analysis, the National Commission on the Future of DNA Evidence mentioned that a general population database "may appeal to those who would like to emphasize individual differences and ignore group differences."[225] The pertinent issue presented by technological advances in forensic DNA analysis, however, is not whether we want to ignore group difference. Rather, it is what justification exists to continue to present DNA evidence in terms of race. It is to this question that we now turn by looking at how race is currently used in presenting forensic DNA evidence in courts of law.

California provides an apt site to pursue this question. From *People v. Barney*[226] in 1992 to *People v. Wilson*[227] in 2006, a series of California cases has played an important role both in reflecting and shaping practices concerning the use of racial data in the presentation of forensic DNA evidence from its early years to the present day. These cases chart a trajectory from the initial rejection of RMPs calculated using broad racial databases[228] to the embrace of racial databases in the aftermath of the NRC II report,[229] the renewed questioning of which databases were appropriate to reference,[230] and, finally, the full embrace of the standardized use of broad racial databases in the calculation and presentation of RMPs to a jury in a criminal case.[231]

A. Early Cases: DNA in Flux

As noted above,[232] the court in *People v. Barney* found that disagreement and uncertainty in the scientific community regarding the selection of appropriate reference populations precluded the admission of DNA evidence based on the product rule.[233] The court discussed not only the findings of the first NRC report but also dealt at length with the 1991 dispute that pinned Lewontin and Hartl against Chakraborty and Kidd in the pages of *Science* over the selection of appropriate reference populations for calculating RMPs.[234] The court then went on to comment on how the first NRC report had taken note of this controversy[235] and

---

225 FUTURE, *supra* note 33, at 27 (emphasis added).

226 10 Cal. Rptr. 2d 731 (Ct. App. 1992).

227 136 P.3d 864 (Cal. 2006).

228 *Barney*, 10 Cal. Rptr. 2d at 743.

229 People v. Soto, 981 P.2d 958, 959-60 (Cal. 1999).

230 People v. Pizarro, 3 Cal. Rptr. 3d 21, 29-30 (2003), *disapproved by* People v. Wilson, 136 P.3d 864 (Cal. 2006).

231 People v. Wilson, 136 P.3d 864, 865-66 (Cal. 2006).

232 *See supra* notes 92, 130 and accompanying text.

233 *Barney*, 10 Cal. Rptr. 2d at 743.

234 *Id.* at 740-41.

235 *Id.*

concluded that because the dispute among experts remained unresolved, the court could not admit into evidence RMPs calculated using the broad racial databases.[236]

People v. Barney was followed by a flurry of discussion and general professional hand-wringing over the need to resolve the disputes so that DNA evidence could be used with impunity.[237] The second NRC report issued in 1996 seemed to settle the argument in favor of Chakraborty and Kidd, opening the door to the free use of racial databases in calculating RMPs.[238] The 1999 California case of *People v. Soto* took note of this development when it effectively overruled *People v. Barney* on the grounds that the scientific community had accepted use of the product rule in DNA forensic evidence.[239]

In *Soto*, the defendant was charged with rape.[240] The court recounted that, although the victim was unable to identify her assailant because he wore a mask, "[s]he described her assailant as a [w]hite male . . . with light or blond hair and an olive complexion."[241] Soto was described as "Latino . . . with a dark complexion and black hair."[242] Nonetheless, DNA from semen left at the crime scene matched Soto's.[243] Using the older RLFP analysis of four genetic loci,[244] Robert Keister, a criminalist at the Orange County Sheriff's Department (OCSD), testified at trial that "there was a probability of 1 in 189 million of finding that same DNA pattern in individuals selected at random from the population represented by the OCSD's Hispanic database."[245] Interestingly, at the preliminary examination before the trial, Keister initially calculated a probability of 1 in 214 million.[246] This difference of well over 10% resulted from "add[ing] some more samples to [the OCSD] database and . . . [running] further tests on the augmented database."[247] No explanation was given for why samples were added, where they came from, or how they were characterized as "Hispanic." Further discussion revealed that Keister also used FBI Hispanic databases to produce the following frequency estimates: "(1) Southwest Hispanic (Texas): 1 in 55 million; (2) Southeast Hispanic (Florida): 1 in 2.3 billion; (3) U.S. Black: 1 in 2.4 billion; and (4) U.S. Caucasian: 1 in 3 billion."[248] Asked to comment on the significance of the variation among frequency estimates, another

---

236 *Id.* at 743.
237 *See supra* notes 92-94 and accompanying text.
238 *See supra* notes 123-126 and accompanying text.
239 People v. Soto, 981 P.2d at 958, 960 (Cal. 1999).
240 *Id.*
241 *Id.* at 961.
242 *Id.*
243 *Id.*
244 *Id.* at 967.
245 *Id.* at 961.
246 *Id.* at 967 n.19.
247 *Id.*
248 *Id.* at 971.

DNA expert witness, Dr. Bruce Kovacs, professor of medicine at University of Southern California, testified that

> [the denominators] are astronomically large numbers. The significance of whether something is 1 in 55 million or 1 in 110 million versus 1 in 4 billion is something that I can't really get my hands on in a real concrete way to distinguish that difference. It's a very, very, very rare event.[249]

In this context it seems clear that the experts are making an implicit distinction between statistical significance and forensic significance. Kenneth Kidd himself testified at the trial and made just such a distinction, which the court found to support the notion that "any difference in estimates over one in a million was pragmatically meaningless."[250] From such detailed discussions of odds ratios using very specific numbers that carry the authority of scientific expertise, the witness ultimately characterized the odds of the match simply as "very, very, very rare"—not particularly scientific terminology, but apparently adequate to aid the relevant finder of fact in making a determination of guilt or innocence.

One might ask why it was acceptable in *Soto* to significantly change frequency estimates by the addition of more racialized data or reference to other databases but apparently unacceptable (or at least not considered) to change frequency estimates by removing race altogether. The *Soto* court's further discussion of the rationale for using racialized databases provides some insight into this issue. Thus, the court noted that

> [m]ajor laboratories that do RFLP analysis . . . have developed their own separate population databases for each of several broad racial or ethnic categories such as Caucasian, Black, and Hispanic, the assumption being that mating among members of any one of those categories of the United States population is sufficiently random to justify using them in conjunction with the product rule to calculate the frequency of a DNA profile.[251]

The assumption of random mating was central to overcoming Lewontin and Hartl's concerns about ethnic substructuring and hence supporting the court's decision to reject the reasoning of the *Barney* court and admit the race-specific frequency estimates into evidence. The court goes on in a footnote, however, to consider and reject the possibility of using a non-racially marked database for calculating RMPs, stating that

> [c]onversely, the laboratories do not use a single interracial United States database, presumably because the incidence of random mating between members of the different racial categories is deemed low enough to preclude

---

249 *Id.* at 972.
250 *Id.* at 973.
251 *Id.* at 967 (citations omitted).

> use of the product rule to calculate an overall frequency statistic for the United States population as a whole.[252]

The characterization of a single general database as "interracial" is in itself notable. It conflates the absence of racial markers assigned to DNA samples with the presence of interracial mating among the sources of such samples. Viewed in this light, the court's characterization of an "interracial" genetic database may be seen as reflecting a much deeper, unarticulated, and misguided understanding of races as biologically distinct in meaningful ways that are perpetuated by mating patterns. Such presumptions reflect Jim Crow-era logic of anti-miscegenation where through either de facto or de jure historical patterns individuals were "deemed" to mate across racial lines in only small numbers.[253] The failings of such an anti-miscegenation logic are evident in the historical reality of interracial mating throughout the country's history[254] and are especially pronounced with respect to the category "Hispanic," which, as Lewontin and Hartl noted in the 1991 *Science* article "is a biological hodgepodge. It includes people of Mexican, Puerto Rican, Guatemalan, Cuban, Spanish, and other ancestries."[255]

However, none of these points were made at trial because the expert witnesses for the defense were still arguing that *more* ethnicity was needed, not less, to calculate RMPs.[256] Thus, one defense expert advocated for "separate databases from the separate ancestral populations that live in places like Cuba, Mexico, Spain, and Central America."[257] This is perhaps still understandable in a case where the older RFLP technique was used to analyze only four genetic loci, but soon this technique would be superseded by PCR analysis of up to thirteen CODIS loci.[258]

B. From Pizarro *to* Wilson*: Race in Flux*

The 2003 case of *People v. Pizarro*[259] marked another major shift in the presentation and use of racially marked forensic DNA evidence in court. Michael Pizarro was convicted of murder and rape in 1990.[260] He

---

[252] *Id.* at 967 n.18.

[253] *See, e.g.*, Peggy Pascoe, *Miscegenation Law, Court Cases, and Ideologies of "Race" in Twentieth-Century America*, 83 J. AM. HIST. 44, 58-60 (1996).

[254] *Id.* Harvard professor Henry Louis Gates, host of the PBS special *African American Lives*, has estimated that "about 30 percent of the African American male population has a white male ancestor." AfricanDNA, *Harvard Professor Henry Louis Gates Joins Forces with Family Tree DNA to Launch AfricanDNA.com* (Nov. 15, 2007), http://www.africandna.com/News.aspx.

[255] Lewontin & Hartl, *supra* note 34, at 1749.

[256] *See Soto*, 981 P.2d at 970.

[257] *Id*. (internal quotation marks omitted).

[258] *See supra* Part III.B, notes 186-187 and accompanying text.

[259] 3 Cal. Rptr. 3d 21 (Ct. App. 2003), *disapproved by* People v. Wilson, 136 P.3d 864 (Cal. 2006).

[260] *Id.* at 28-29.

appealed the case in 1992 on the grounds that the prosecution did not prove that RFLP testing of DNA evidence was at that time "generally accepted in the scientific community."[261] The case was remanded for a "thorough evidentiary hearing," which occurred in 1998 (by which time such issues were largely resolved in the scientific community[262]), and the court "ruled that the evidence was admissible and reentered the judgment."[263]

In this second appeal, Pizarro contended that there was a basic error in the presentation of the DNA evidence when the prosecution informed the jury "that the DNA profile frequency . . . was the probability of finding a matching profile in the *Hispanic* population."[264] Pizarro himself was identified as Hispanic, but the ethnic identity of the perpetrator was not known independently.[265] The court ruled in Pizarro's favor, finding that the use of the Hispanic database presumed that the perpetrator was in fact Hispanic.[266] Nevertheless, the court did not decide "whether there was sufficient evidence to conclude the perpetrator in this case was Hispanic."[267] It also concluded that "recurring thematically throughout the issues in this case are evidentiary violations founded on the improper assumption that the *defendant was in fact the perpetrator* and that the defendant's traits therefore could be relied upon to provide or clarify those traits of the perpetrator forming the basis of the DNA evidence."[268] The court argued that "in the absence of sufficient evidence of the perpetrator's ethnicity, *any* particular ethnic frequency is irrelevant"[269] and found that "the improper mention of ethnicity unfairly and unjustifiably encourages the jurors to focus on ethnicity and race—specifically the ethnicity and race of the defendant, the only suspect before them."[270]

In a footnote, the court presented three options that prosecutors have for presenting profile frequencies:

> (1) establish that the perpetrator more likely than not belongs to a particular ethnic population, then present only the frequency in that particular ethnic population; (2) present only the most conservative frequency, without mention of ethnicity; or (3) present the frequency in the general, nonethnic population. These options promote the goals of admitting only relevant evidence and

---

261 *Id.* at 29.
262 *See* Aronson, *supra* note 57, at 173-75.
263 *Pizarro*, 3 Cal. Rptr. 3d at 29.
264 *Id.* at 97.
265 *Id.*
266 *Id.*
267 *Id.*
268 *Id.* at 29.
269 *Id.* at 104.
270 *Id.* at 105.

> eliminating unjustifiable and potentially prejudicial references to ethnicity and race.[271]

The court here seemed to be acutely sensitive to the dangers of improperly injecting race into the presentation of DNA evidence. Significantly, it broached the possibility of moving beyond race in the presentation of frequencies. Nonetheless, it remained primarily concerned with the proper management of racial references and did not go on specifically to question the underlying utility (or lack thereof) of race itself as an analytic category in the presentation of DNA evidence.

In the course of reaching this conclusion, the court's opinion presents some revealing discussions of the meaning and significance of race in forensic DNA analysis. For example, as the court noted, the State argued that any reference to race was harmless in part because "frequencies do not vary greatly by ethnicity."[272] This, of course, raises the issue of why one should use ethnicity (or race) at all if the differences are so insignificant. Indeed, here it becomes clear that under such circumstances *the only thing that race adds to the presentation of such DNA evidence is race itself*—not simply as a marker of the suspect, but as a conceptual framework for constructing a relationship among violent crime, genetics, and race.

At the 1990 trial, the only scientific witness testified that "[t]he likelihood of finding another unrelated Hispanic individual with a similar profile as Mr. Pizarro is one in approximately 250,000."[273] Such odds fall well below 1 in 1,000,000, beyond which geneticist Kenneth Kidd saw no pragmatic significance;[274] hence, they may seem to justify the use of a different racial database in this case. It turns out, however, that Pizarro was actually identified as "half Hispanic and half Caucasian."[275] When asked how he could calculate RMPs in such a situation, the expert in the original trial stated that "there is nothing we can do other than to compare them to the two populations and we would use only the smaller of the two in our report. . . . [Using the smaller population] is less detrimental to the defendant."[276] Pizarro's "mixed" race presented a problem for the witness. (It certainly flies in the face of the anti-miscegenation logic of *Soto*.[277]) Analytically, the expert literally *segregated* Pizarro's racial identities, producing separate RMPs with reference to distinct White and Hispanic databases. His conceptual framework could not encompass the concept of mixed race—rather it was premised upon, and indeed demanded, a logic of racial purity.

---

271 *Id.* at 105 n.85.
272 *Id.* at 97.
273 *Id.* at 97-98 (emphasis omitted).
274 *See infra* text accompanying notes 305-306.
275 *See Pizzaro*, 3 Cal. Rptr. 3d at 104 n.81 (emphasis omitted).
276 *Id.* (emphasis omitted).
277 *See supra* text accompanying notes 252-255.

In the aftermath of *Pizarro*, David Kaye wrote a powerful and influential critique of the court's reasoning regarding the use of ethnic reference populations in calculating RMPs.[278] Kaye essentially agreed with the *Pizarro* court that "[i]f the perpetrator could have come from any of several racial groups, looking to only one racial group for a random match probability could be misleading."[279] He expressed grave concern, however, over the court's conclusion that "giving a range of frequencies for the major racial or ethnic groups in the United States [was therefore] unacceptable."[280] Kaye noted, "Since providing statistics from several racial groups is the standard way of assessing the significance of a match in cases in which the racial and ethnic status of the perpetrator of the crime initially is unknown, the opinion [in *Pizarro*] casts doubt on the outcomes of innumerable cases."[281] Kaye disputed what he saw as the court's presentation of an "unbridgeable gap between scientific and legal reasoning in this situation,"[282] asserting that

> the scientific reasoning that the court questioned is nothing less than the kind of hypothesis testing—considering the principal alternatives and examining the probability of certain outcomes under each of these alternative hypotheses—that dominates modern statistical thinking. In this instance, the DNA expert simply testifies to how surprising the match would be if some major alternatives to the hypothesis that the defendant is the source of the biological samples were true.[283]

Kaye concluded that, with respect to considerations of logical relevance, "it is difficult to conceive of any substantive difference between legal and scientific reasoning."[284] In the abstract, there is much merit to Kaye's argument. But in declaring no difference between scientific and legal *reasoning*, he obscured the distinction between scientific and legal *relevance*.

When noting that a perpetrator may "share the defendant's race or ethnicity" Kaye conflates race and genetics by referring to a defendant's "genetic heritage."[285] The concept of "sharing" is very peculiar and particular here. *Pizarro* involved someone who Kaye and the court define as "half Hispanic" and "half Caucasian"—implicitly making these two categories mutually exclusive. Yet in social practice this makes no sense and reinforces the idea of genetically distinct and bound "races" rather than continuums of variable "mixes." Michael Pizarro could not be allowed to be a "Hispanic Caucasian" because the databases are not constructed that way. Two suspects may "share" the

---

278 *See generally Logical Relevance*, *supra* note 50.
279 *Id.* at 214.
280 *Id.*
281 *Id.*
282 *Id.*
283 *Id.* (footnote omitted).
284 *Id.* at 215.
285 *Id.* at 212.

same race, but that "race" itself must be singular and unmixed—not "shared" with other races, but rather capable of being broken down into parts "half x" and "half y." In short, the entire model of using race to improve probability estimates depends on keeping genetic databases segregated by race. The segregation in turn produces RMPs.

Kaye correctly noted that there was no necessary presumption made about a perpetrator's identity if the suspect's DNA was compared to an array of racial databases of populations to which the perpetrator *might* belong.[286] He therefore adequately addressed and effectively undermined two of the *Pizarro* court's three permissible options for the presentation of profile frequencies: "(1) establish that the perpetrator more likely than not belongs to a particular ethnic population, then present only the frequency in that particular ethnic population; [and] (2) present only the most conservative frequency, without mention of ethnicity . . . ."[287] Kaye's logic, however, was based on a presumption that race itself remained relevant in the calculation of RMPs. Thus, it failed to address the third option to "present the frequency in the general, non-ethnic population."[288]

In the 2006 case of *People v. Wilson*, the California Supreme Court embraced Kaye's arguments to disapprove of the reasoning in *Pizarro* and re-validate the calculation of RMPs using race-specific databases even when the race of the perpetrator is not otherwise known.[289] In reaching its conclusions, the court asserted that "[t]he question here revolves around exactly what is the relevant population. The question is complicated by the fact that the odds vary with different racial and ethnic groups. Because of this variation, separate databases are maintained for different population groups, and the odds for each group are calculated separately."[290] The court then agreed with the lower court's finding that "[w]hen the perpetrator's race is unknown, the frequencies with which the matched profile occurs in various racial groups to which the perpetrator *might* belong are relevant for the purpose of ascertaining the rarity of the profile."[291] This effectively overturned *Pizarro* and reinstated the practice of using racially marked databases to generate profile frequencies.

VI. RACE, GENES, AND RELEVANCE

Considered in light of the above discussion, it is now clear that the use of race in generating RMPs for forensic DNA matches should be deemed inadmissible by courts as neither relevant nor reliable. The

---

286 *See id.* at 214.
287 People v. Pizzaro, 3 Cal. Rptr. 3d 21, 105 n.85 (Ct. App. 2003).
288 *Id.*
289 *See* People v. Wilson, 136 P.3d 864, 868-69 (Cal. 2006).
290 *Id.* at 865-66.
291 *Id.* at 866.

Supreme Court notably articulated a "gatekeeping" role for the trial court judge in considering the admissibility of scientific evidence in the 1993 case of *Daubert v. Merrell Dow Pharmaceuticals, Inc*.[292] Central to the holding in *Daubert* was the Court's articulation of a requirement that the trial judge ensure that "an expert's testimony both rests on a reliable foundation and is relevant to the task at hand."[293]

A. When Race Is Not Relevant

Federal Rule of Evidence ("FRE") 401 states that "'[r]elevant evidence' means evidence having any tendency to make the existence of any fact that is of consequence to the determination of the action more probable or less probable than it would be without the evidence."[294] Clearly forensic DNA evidence is often relevant to a criminal proceeding. RMPs generated through reference to a population database are therefore also often relevant. A central argument of this Article, however, is that in the presentation of such RMPs, race is *not* relevant. Race does not add information that has "any tendency to make the existence of any fact that is of consequence to the determination of the action more probable or less probable than it would be without the evidence."[295]

Taking the *Wilson* case as a paradigmatic example of how race is used in the presentation of forensic DNA evidence, we can see that central to the court's decision were the assumptions it brought to bear regarding the relevance of race in producing DNA evidence. Following the lower court's assertion that racial data is relevant,[296] the court made the relatively straightforward assertion that "[r]elevant evidence is evidence 'having any tendency in reason to prove or disprove any disputed fact that is of consequence to the determination of the action.'"[297] The court went on to note that "[t]he test of relevance is whether the evidence tends, 'logically, naturally, and by reasonable inference' to establish material facts such as identity, intent, or motive."[298] These are basic rules of evidence and consistent with the FRE 401 concept of relevance. The court, however, framed the question of relevance in terms of "what is the relevant population" rather than considering whether differentiation among populations itself provided any *legally* relevant data.[299] In Wilson's case, and in most cases using

---

292 509 U.S. 579 (1993).
293 *Id.* at 597.
294 FED. R. EVID. 401.
295 *Id.*
296 *Wilson*, 136 P.3d at 869.
297 *Id.* (quoting CAL. EVID. CODE § 210).
298 *Id.* (citation omitted).
299 *Id.* at 865.

current techniques of forensic DNA analysis, the answer to this latter question should simply be *no*.

The RMPs at issue in *Wilson* ranged from "one of 96 billion Caucasians, one of 180 billion Hispanics, and one of 340 billion African-Americans."[300] The court accepted this racially marked data as relevant because forensic scientists had identified statistically significant variation in frequencies when using different racial reference populations to generate RMPs.[301] The court went on to quote approvingly Professor Kaye's assertion that, "[c]ontrary to the *Pizarro* court's assertions, in a 'general population case'—one in which the investigation cannot be limited to a particular racial group—the statistics for a range of groups surely are relevant."[302] Kaye made the apparently reasonable point that having more data about RMPs for a range of populations would "surely" aid a jury in establishing a material fact, such as identity.[303] And indeed, the court concluded that "[i]t is relevant for the jury to know that most persons of at least major portions of the general population could not have left the evidence samples."[304]

But forensic (and other) scientists have also repeatedly made the point that once a particular odds threshold is passed, any difference among profile frequencies is of little or no practical significance.[305] As the court noted in the 1999 *Soto* case, Yale geneticist Kenneth Kidd had provided support for the conclusion that "any difference in estimates over one in a million was pragmatically meaningless."[306] Moreover, as the *Wilson* court explained based on its understanding of Nicola Shea's testimony, "[w]hen nine genetic markers are used in the analysis, the result would be a pretty discriminating number no matter what population data base was used."[307] Yet at no point did the court consider the logical implication of Shea's statement—that under such circumstances, using racially marked databases to generate RMPs added nothing to the ability of the jury to make determination of guilt or innocence. The difference between one in 96 billion and one in 340 billion simply does *not* "hav[e] any tendency in reason to prove or disprove any disputed fact that is of consequence to the determination of the action."[308] Such information provides nothing of use to the finder of fact that would not already be available by using a general non-racially marked reference population, which would have generated similarly powerful RMPs. In other words, where experts can generate such

---

300 *Id*. at 867.
301 *See id.* at 865-66.
302 *Id.* at 869 (citation omitted).
303 *Id.*
304 *Id.*
305 *See supra* notes 96-97, 107-108 and accompanying text.
306 People v. Soto, 981 P.2d 958, 973 (Cal. 1999).
307 *Wilson*, 136 P.3d at 867 (internal quotation marks omitted).
308 *Id.* at 869 (internal quotation marks and citation omitted).

astronomically low RMPs, race simply is *irrelevant* and should not play a role in the presentation of DNA evidence.

Several other statements by prominent forensic DNA experts further highlight the glaring irrelevance of race for presenting DNA evidence given the power of current technology. Arguing in 1996 for the adequacy of using broad racial databases to generate RMPs, the FBI's own Bruce Budowle and Keith Monson noted that "[a] profile would be considered rare whether it has an estimated frequency of 1/5,000,000, 1/50,000,000, or 1/500,000,000. Obviously, the difference in the rarity of such estimates would have little consequence in a forensic context."[309] More to the point, Budowle and Eric Lander, in their highly influential 1994 *Nature* article on forensic DNA technology, argued that a distinction in population frequency between "10^{-5} or 10^{-7}" was "irrelevant for courtroom use."[310] The distinction in population frequencies across the diverse race-specific RMPs generated in *Wilson* (roughly between 10^{-11} and 3.4×10^{-11}) was far smaller than that cited by Budowle and Lander as irrelevant. Given that current techniques regularly generate RMPs in the range of 10^{-11} (1 in 1,000,000,000,000)[311] across diverse racial databases, any distinction among race-specific RMPs must be understood as similarly of "little consequence in a forensic context"[312] and hence "irrelevant for courtroom use."[313] In forensic contexts, the only thing that race adds to RMPs is race itself. It provides no additional information that is relevant to aiding the finder of fact to resolve any material issue at trial.

B. When Race Is Not Reliable

The requirement that scientific evidence be "reliable" is typically discussed in terms of the following factors set forth in *Daubert*: (1) whether the technique or theory underlying the evidence has been tested;[314] (2) whether "[it] has been subject[] to peer review and publication;"[315] (3) "the known or potential rate of error" of the technique or theory when applied;[316] (4) "the existence and maintenance of standards [or] control[s];"[317] and (5) whether the technique or theory has been generally accepted in the scientific community.[318]

---

[309] Bruce Budowle & Keith L. Monson, Accepted Practices by the Forensic DNA Community Supported by NRC II Report, http://www.promega.com/geneticidproc/ussymp7proc/0703.html (last visited Jan. 28, 2009) (citations omitted).

[310] Lander & Budowle, *supra* note 95, at 738.

[311] *See*, *e.g.*, BUTLER, *supra* note 3, at 94-95; *see* Budowle et al., s*upra* note 17.

[312] Budowle & Monson, *supra* note 309.

[313] Lander & Budowle, *supra* note 95, at 738.

[314] Daubert v. Merrell Dow Pharm., Inc., 509 U.S. 579, 593 (1993).

[315] *Id.* at 593-94.

[316] *Id.* at 594.

[317] *Id.*

[318] *Id.*

When looking at these factors in relation to the generation and presentation of race-specific RMPs for DNA evidence, it is immediately clear that factors (1), (2), and (5) have been met. As discussed above, over the years, numerous studies have been published in peer reviewed journals testing and evaluating the use of race-specific databases to generate RMPs.[319] Thus, since the inception of forensic DNA evidence, the use of race has been standard and generally accepted practice.[320] Such general acceptance, however, is no longer the sole determining factor in assessing the reliability of scientific evidence. When scientific practices concerning the use of race in relation to forensic DNA are examined more closely, it becomes evident that they fail to meet factors (3) and (4): there has been little or no consideration of potential rates of error regarding the definition of race and its assignment to particular DNA samples, nor are there adequate standards or controls for the definition and assignment of racial categories to DNA samples.[321] Such lack of basic scientific rigor calls into question the reliability of RMPs generated using racial categories.

Specifically, in the context of forensic DNA research, we see that the scientists who have developed racialized databases have in effect let the concept of "self-identification" supplant the need for any scientifically rigorous or coherent rationale for classifying genetic data by race. This is apparent in the highly influential article written by Budowle et al. in 2001, which has become a primary reference in calculating race-specific RMPs.[322] Titled *CODIS STR Loci Data from 41 Sample Populations*,[323] the Budowle article purports to "present[] STR allele distribution data on 12 or 13 of the CODIS core STR loci in several sampled populations from each of the following major population groups: African Americans, U.S. Caucasians, Hispanics, Far East Asians, and Native Americans."[324] This distribution data was derived from samples provided by twenty laboratories distributed widely across the U.S., Canada, the Caribbean, and Mexico.[325]

Like the Vallone et al. article discussed above,[326] the Budowle article takes care to specify the technical laboratory instruments and practices used to analyze the samples.[327] But with regard to race, Budowle et al. fall below even the Vallone et al. article's meager

---

[319] *See, e.g.*, *supra* notes 33-34, 39, 84, 159-160 and accompanying text.

[320] *See supra* notes 63-87 and accompanying text.

[321] *See supra* notes 163-168 and accompanying text, and *infra* notes 322-336 and accompanying text.

[322] E-mail from John Butler, leader of the NIST Human Identity Project Team, to Jonathan Kahn, Associate Professor of Law, Hamline University School of Law (Apr. 26, 2007, 2:47 p.m.) (on file with author).

[323] Budowle, *CODIS STR Loci Data*, *supra* note 159.

[324] *Id.* at 453.

[325] *Id.*

[326] *See supra* Part IV.A.

[327] *See* Budowle, *CODIS STR Loci Data*, *supra* note 159, at 453, 459.

reference to self-identification[328] and provide absolutely no information on how or by whom racial identity was ascribed to these samples. Most of the samples came from law enforcement agencies.[329] Self-identification may have been used, but it is also quite likely that law enforcement authorities themselves ascribed racial identities to the samples.

In an article on the ethical, legal, and social implication of forensic DNA analysis, Mildred Cho and Pamela Sankar discuss at length a British study showing that external ascriptions of racial identity by law enforcement authorities correspond very poorly with underlying patterns of genetic variation.[330] The article notes that in the British study, "[c]lassifications into the five 'ethnic' groups [Caucasian, Afro-Caribbean, Indian sub-continental, Southeast Asian, and Middle Eastern] were assigned by police officers by visual characteristics, . . . based on [perceptions of outward] appearance rather than any knowledge of an individual's ancestry."[331] The actual correspondence of these external ascriptions to the "true" ancestry of the individuals ranged from 30% for the Middle Eastern category up to 67% for Afro-Caribbean, with Caucasian falling at 56%.[332] In other words, if the samples providing the basis for the Budowle article were classified based on external ascriptions of race by law enforcement authorities, it would not be unreasonable to suppose that somewhere around 50% of the classifications were inaccurate in terms of their relation to genetically based ancestral origins. If this is the case, it calls into question the legitimacy of any RMPs derived from these reference populations.

Perhaps the samples provided to Budowle were classified by self-identification. This, however, would not solve the problem. Self-identification is a *social*, not *genetic*, practice.[333] Moreover, as Cho and Sankar note, "individual self-classification is not stable; for example, one US study found that one-third of people change their own self-identified race or ethnicity in two consecutive years."[334] Complicating matters still further, a recent study by Condit et al. found people often have very "incomplete knowledge of their [biological] ancestry."[335] Among the subjects interviewed for a study on attitudes toward race-based pharmacogenomics (the tailoring of drugs to genetic profiles), Condit

---

[328] *See* Vallone et al., *supra* note 164, at 279.

[329] Budowle, *CODIS STR Loci Data*, *supra* note 159, at 453.

[330] *Forensic Genetics*, *supra* note 13, at S10.

[331] *Id.* (citing A. Lowe et al., *Inferring Ethnic Origin by Means of an STR Profile*, 119 FORENSIC SCI. INT'L 17 (2001)) (internal quotation marks omitted).

[332] *Id.* (citing A. Lowe et al., *Inferring Ethnic Origin by Means of an STR Profile*, 119 FORENSIC SCI. INT'L 17 (2001)).

[333] *See id.* at S9.

[334] *Id.* (citing K. Leech, *A Question in Dispute: The Debate About an "Ethnic" Question in the Census*, *in* RUNNYMEDE RES. REP. (1989)).

[335] Celeste Condit et al., *Attitudinal Barriers to Delivery of Race-Targeted Pharmacogenomics Among Informed Lay Persons*, 5 GENETICS IN MED. 385, 385 (2003).

found that "39.6% did not know all four of their [biological] grandparents."[336] In such situations, self-declared race may fail to capture significant variations in biological ancestry.

This lack of care given to the meaning and attribution of race in a genetic context contrasts markedly with the obvious scientific rigor applied to the elaboration of the more technical aspects concerning the extraction, amplification, and analysis of forensic DNA samples.[337] Clearly, the general practice of using forensic DNA to help identify criminal suspects meets all the *Daubert* standards of reliability. It is only with respect to the handling of race that the reliability of particular RMPs should be called into question. The use of a general reference population to generate RMPs without regard to race would directly overcome this lack of reliability.

C. Race, Genes, and Prejudice

Even if race-specific RMPs were deemed somehow relevant and reliable, they should still be excluded as unduly prejudicial. FRE 403 states,

> Although relevant, evidence may be excluded if its probative value is substantially outweighed by the danger of unfair prejudice, confusion of the issues, or misleading the jury, or by considerations of undue delay, waste of time, or needless presentation of cumulative evidence.[338]

The probative value of race-specific RMPs must be evaluated in relation to the alternative probative value of non-race-specific RMPs. As noted above,[339] Yale geneticist Kenneth Kidd testified in *People v. Soto* that once the odds threshold of one in one million was crossed, any further differentiation among RMPs was what the court called "pragmatically meaningless."[340] Similarly, the FBI's Bruce Budowle and Keith Monson discussed the difference between odds of 1 in 5,000,000 and 1 in 500,000,000 as of little or no forensic significance.[341] Since current technology can use non-racial general reference populations to regularly generate RMPs far in excess of 1 in 5,000,000 (and even in excess of 1 in 500,000,000), the probative value of any refinement of the odds provided by the addition of race-specific RMPs, even if relevant, should be deemed de minimis.

What concerns for prejudice should then be balanced in the scales against this de minimis relevance? The dangers of racial bias

---

[336] *Id.* at 388. The two reported studies had population sizes of 104 and 120 participants. *Id.* at 385.

[337] *See supra* Part IV.A.

[338] FED. R. EVID. 403.

[339] *See supra* note 250 and accompanying text.

[340] People v. Soto, 981 P.2d 958, 973 (Cal. 1999).

[341] *See* Budowle & Monson, *supra* note 309.

tainting the evaluation of forensic evidence should be of paramount concern in this context. DNA evidence is usually presented in cases of violent crimes, often of the most heinous variety.[342] Where race is gratuitously injected into the context of violent crime and genetics is added to the mix, the danger of creating stigmatizing racial stereotypes by conflating race, violence, and genes[343] should be deemed to outweigh any *de minimis* probative value provided by race-specific RMPs.

Concern to ensure that racial prejudice does not infect the justice system must be primary in any evaluation of the admissibility of forensic DNA evidence. As the U.S. Supreme Court noted in *McCleskey v. Kemp*, "[b]ecause of the risk that the factor of race may enter the criminal justice process, we have engaged in unceasing efforts to eradicate racial prejudice from our criminal justice system."[344] Thus, for example, the prosecution may not challenge a juror on the basis of race;[345] a change of venue may be constitutionally required as a result of widespread bias in a community;[346] and the prosecution is barred from appealing to racial prejudice in its argument to the jury.[347]

In their treatise on Federal Practice and Procedure, Wright and Graham note that "any reference to race by prosecutor must be justified by compelling state interest."[348] They caution, in particular, that "[w]hile many jurors would reject crude appeals to prejudice, more sophisticated forms of this technique may not be recognized as such. *Today the appeal to prejudice is apt to be disguised as some form of science*."[349] With specific reference to FRE 403, they conclude that

> fairness in adjudication does not consist entirely in the accuracy of the factual determinations but may require some sacrifice of accuracy to avoid the suspicion that the decision rests on prejudice disguised as science. Therefore, the party who asserts a major premise based on one of the suspect classifications must expect that his premise will be more rigorously scrutinized than is typical in rulings on relevance.[350]

---

[342] Jeffrey M. Prottas & Alice A. Noble, *Use of Forensic DNA Evidence in Prosecutors' Offices*, 35 J.L. MED. & ETHICS 310, 312 (2007) ("DNA evidence is most often used in sexual assault cases. It appears to play a role in a significant minority of murder cases and is rarely employed otherwise.").

[343] For a broad discussion of the phenomenon, see Karen Rothenberg & Alice Wang, *The Scarlet Gene: Behavioral Genetics, Criminal Law, and Racial and Ethnic Stigma*, 69 L. & CONTEMP. PROBS. 343, 361-64 (2006).

[344] McCleskey v. Kemp, 481 U.S. 279, 309 (1987) (internal citation and quotation marks omitted).

[345] Batson v. Kentucky, 476 U.S. 79, 85-86 (1986).

[346] Irvin v. Dowd, 366 U.S. 717, 728 (1961).

[347] *See, e.g.*, People v. Cudjo, 863 P.2d 635, 661 (Cal. 1993).

[348] 22 CHARLES ALAN WRIGHT & KENNETH W. GRAHAM, JR., FEDERAL PRACTICE AND PROCEDURE § 5179, at 237 n.11 (Supp. 2008) (citing McFarland v. Smith, 611 F.2d 414, 417 (2d Cir. 1979)).

[349] 22 CHARLES ALAN WRIGHT & KENNETH W. GRAHAM, JR., FEDERAL PRACTICE AND PROCEDURE § 5179, at 162-63 (1978) (footnote omitted and emphasis added).

[350] *Id.* § 5179, at 163 (footnote omitted).

Thus far, the use of race in the presentation of forensic DNA evidence has received virtually no scrutiny from courts in terms of the value or lack thereof that race adds to the accuracy of the RMPs thus generated. Wright and Graham allow that some measure of accuracy may need to be sacrificed to avoid the suspicion of racial prejudice.[351] In the case of presenting RMPs without regard to race, such a sacrifice would be negligible.

Wright and Graham's reference to the distinctive power of science to disguise appeals to prejudice[352] is especially apt in the context of forensic DNA evidence. In a study of mock jurors, Jonathan Koehler found that "the way in which DNA match statistics are framed and presented to legal fact finders may affect how they think about and use the DNA evidence."[353] Koehler's study looked only at different probabilistic frames for presenting the same statistic,[354] but it is important to consider that similar subtle psychological dynamics may be at work in the framing of RMPs in terms of race.

Sheri Lynn Johnson has argued that the use of negative racial stereotypes pervades the presentation of criminal cases to juries.[355] She argues that "[i]f the entire body of relevant data is surveyed, the inference that race influences many white jurors' determinations of guilt is unavoidable."[356] In their recent article, *Implicit Bias: Scientific Foundations*,[357] Anthony Greenwald and Linda Krieger discuss the "science of implicit cognition," which "suggests that actors do not always have conscious, intentional control over the processes of social perception, impression formation, and judgment that motivate their actions."[358] They define "implicit biases" as "discriminatory biases based on implicit attitudes or implicit stereotypes."[359] Being implicit, such biases are not conscious—yet they are significant. They note that

> [i]mplicit biases are especially intriguing, and also especially problematic, because they can produce behavior that diverges from a person's avowed or endorsed beliefs or principles. The very existence of implicit bias poses a challenge to legal theory and practice, because discrimination doctrine is premised on the assumption that, barring insanity or mental incompetence,

---

[351] *Id.*

[352] *Id.*

[353] Jonathan J. Koehler, *The Psychology of Numbers in the Courtroom: How to Make DNA-Match Statistics Seem Impressive or Insufficient*, 74 S. CAL. L. REV. 1275, 1277 (2001).

[354] *Id.* at 1277-78.

[355] Sheri Lynn Johnson, *Racial Imagery in Criminal Cases*, 67 TUL. L. REV. 1739 *passim* (1993).

[356] *Id.* at 1804.

[357] Anthony G. Greenwald & Linda Hamilton Krieger, *Implicit Bias: Scientific Foundations*, 94 CAL. L. REV. 945 (2006).

[358] *Id.* at 946.

[359] *Id.* at 951.

> human actors are guided by their avowed (explicit) beliefs, attitudes, and intentions.[360]

Greenwald and Krieger go on to review data from the "Implicit Association Test," which is widely used to "assess[] implicit attitudes toward African Americans[] relative to European Americans[]."[361] They observe that researchers have consistently found what they describe as "implicit attitudinal preference" for European Americans over African Americans.[362] They conclude that "a substantial and actively accumulating body of research evidence establishes that implicit race bias is pervasive and is associated with discrimination against African Americans."[363] To the extent that such implicit race bias might already be present among average jurors, injecting race into the presentation of forensic DNA evidence presents a significant danger of tainting the proceedings with unfair prejudice.

This danger is heightened by the pervasive association of race and violent crime in the public mind.[364] For example, John Hurwitz and Mark Peffley argue that since the infamous "Willie Horton" ad run by the National Security Political Action Committee (NSPAC) against

---

[360] *Id.*

[361] *Id.* at 952.

[362] *Id.* at 953.

[363] *Id.* at 966; *see also* Kristin Lane et al., *Implicit Social Cognition and Law*, 3 ANN. REV. L. & SOC. SCI. 427 (2007). For example, the authors note,

> [i]n both concurring and dissenting opinions, the Supreme Court has acknowledged the potential for implicit bias to impede justice. For example, in her dissent in *Adarand Constructors, Inc. v. Peña* (1995), Justice Ginsburg noted that "[b]ias both conscious and unconscious, reflecting traditional and unexamined habits of thought, keeps up barriers that must come down if equal opportunity and nondiscrimination are ever genuinely to become this country's law and practice." She echoed these sentiments in the University of Michigan affirmative action cases, quoting these precise words in her dissent in *Gratz v. Bollinger* (2003), and writing in her concurring opinion in *Grutter v. Bollinger* (2003), that "[i]t is well documented that conscious and unconscious race bias, even rank discrimination based on race, remain alive in our land, impeding realization of our highest values and ideals."
>
> More specifically, the Court has speculated that implicit bias may affect the perceptions of participants in the legal system: In *Batson v. Kentucky* (1989), Justice Marshall suggested in his concurring opinion that "[a] prosecutor's own conscious or unconscious racism may lead him easily to the conclusion that a prospective black juror is 'sullen,' or 'distant,' a characterization that would not have come to his mind if a white juror had acted identically." Justice O'Connor voiced a similar concern in her dissent in *Georgia v. McCollum* (1992), noting "[i]t is by now clear that conscious and unconscious racism can affect the way white jurors perceive minority defendants and the facts presented at their trials, perhaps determining the verdict of guilt or innocence."

Id. at 442.

[364] The literature on this phenomenon is extensive. *See generally* ROBERT M. ENTMAN & ANDREW ROJECKI, THE BLACK IMAGE IN THE WHITE MIND: MEDIA AND RACE IN AMERICA (2001); Franklin D. Gilliam, Jr. & Shanto Iyengar, *Prime Suspects: The Influence of Local Television News on the Viewing Public*, 44 AM. J. POL. SCI. 560 (2000); Jon Hurwitz & Mark Peffley, *Public Perceptions of Race and Crime: The Role of Racial Stereotypes*, 41 AM. J. POL. SCI 375 (1997); Mark Peffley et al., *Racial Stereotypes and Whites' Political Views of Blacks in the Context of Welfare and Crime*, 41 AM. J. POL. SCI. 30 (1997).

Democrat Michael Dukakis during the 1988 presidential campaign, subtly associating race and crime has been a staple of modern politics.[365] In that spot,

> the narrator [notes] . . . that Willie Horton, a convicted murderer, received multiple weekend furlough passes from prison, during the last of which, the narrator informs us, he "fled, kidnapping a young couple, stabbing the man and repeatedly raping his girlfriend." While the ad could have conveyed exactly the same information without graphics, NSPAC elected to superimpose the most menacing possible picture of Horton, an African American, over the narrative.[366]

Hurwitz and Peffley go on to note that the ad was particularly effective because of its "implicitness," which allowed White Americans to internalize the association of African-Americans and violent crime without directly challenging their conscious commitments to "norm[s] of [racial] equality."[367] Professor of Theology Ted Peters further cautions that "[i]f we identify crime with genes and then genes with race, then we may inadvertently provide a biological support for prejudice and discrimination."[368]

Taken together, the presence of racial imagery in criminal trials, the psychological dynamics of implicit prejudice, and the prominent association of race and violent crime in the public mind all counsel strongly against the unnecessary introduction of race into the presentation of forensic DNA evidence. More specifically, the dangers they present of infecting criminal proceedings with racial bias clearly outweigh the minimal probative value provided by the use of race-specific RMPs. Thus, even if courts deem race-specific RMPs to be relevant, they should nonetheless exclude such evidence as unduly prejudicial.

VII. CONCLUSION

Race has been present in forensic DNA evidence since its inception. Over the past twenty years, the use of race-specific RMPs has become a normative, routine, and largely unquestioned practice. Whatever justifications may have originally been proffered for this practice have long since been superseded by basic technological developments that allow for the calculation of extremely powerful RMPs without reference to race. In relation to the presentation of forensic DNA evidence to juries, race is simply a concept whose time has passed. Race-specific RMPs provide little or no relevant information to finders of fact.

---

[365] *See* Jon Hurwitz & Mark Peffley, *Playing the Race Card in the Post-Willie Horton Era*, 69 PUB. OPINION Q. 99 (2005).

[366] *Id.* at 100.

[367] *Id.* at 100-01.

[368] TED PETERS, PLAYING GOD? GENETIC DETERMINISM AND HUMAN FREEDOM 73 (2d ed. 2003).

They present a significant danger of unfairly prejudicing deliberations through the gratuitous association of race with genetics and violent crime. Ending the practice of generating race-specific RMPs will not materially impede the ability of law enforcement to obtain convictions using DNA evidence. Forensic experts will still be able to regularly generate astronomically low RMPs (often with denominators far in excess of the world's population) using a non-differentiated general reference population. Defendants will not be disadvantaged because race-specific RMPs will only be excluded when they add nothing of substance to the finder of fact's ability to make an informed judgment regarding the DNA evidence. Thus, there is no legal or practical justification for the continued presentation of forensic DNA evidence in terms of race. The practice can and should be ended. It should be replaced with the use of non-racial general population databases to generate RMPs. Indeed, David Kaye has recently noted that such an approach, while statistically more complex than using the current racially differentiated databases, is certainly technically feasible.[369]

Given current technical ability to generate minuscule RMPs, even using a general population base, these recommendations may not change the specific outcomes of individual cases. They will, however, affect larger issues of how the criminal justice system is implicated in constructing, perpetuating, or deepening broader racialized understandings of the relations among race, genetics, and violent crime. By eliminating at least one powerful site for the improper use of genetics as a prism through which to view race and crime, these recommendations aim to take a step toward developing a more appropriate understanding of the complex relations among race, genes, and justice.

---

[369] D.H. Kaye, *The Role of Race in DNA Statistics: What Experts Say, What California Courts Allow*, 37 SW. U. L. REV. 303, 321 (2008).